155454

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From: Chernyshev, Olga
Sent: Saturday, June 04, 2005 12:48 PM
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Subject: 09/869,486; sequence search request

US case 09/869,486

Please search SEQ ID NO: 25, SEQ ID NO: 29 (full length and fragment 73-3714) and SEQ ID NO: 30 in regular and pending databases.
Thank you very much!

Olga N. Chernyshev, Ph.D.
AU 1646
REM 3C89
2-0870
mail 4C70

****
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:____
Date Completed:_____
Searcher Prep/Rev. Time:___
Online Time:_____

****
Type of Search

NA#:_____ AA#:_____
Interference:____ SPDI:___
S/L:_____ Oligomer:____
Encode/Transl:_____
Structure#:_____ Text:___
Inventor:____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 18:12:43 ; Search time 235.801 Seconds
(without alignments)
15127.524 Million cell updates/sec

Title: US-09-869-486B-25
Perfect score: 2180
Sequence: 1 tcgaggccaagaattcggca.....ggaaataaagccatttcaga 2180

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1149.8	52.7	1524	3	US-09-020-956-109	Sequence 109, App
2	1149.8	52.7	1524	3	US-09-030-607-109	Sequence 109, App
3	1149.8	52.7	1524	3	US-09-439-313-109	Sequence 109, App
4	1149.8	52.7	1524	3	US-09-352-616A-109	Sequence 109, App
5	1149.8	52.7	1524	3	US-09-232-149A-109	Sequence 109, App
6	1149.8	52.7	1524	4	US-09-159-812-109	Sequence 109, App
7	1149.8	52.7	1524	4	US-09-636-215-109	Sequence 109, App
8	1149.8	52.7	1524	4	US-09-685-166A-109	Sequence 109, App
9	1149.8	52.7	1524	4	US-09-115-453-109	Sequence 109, App
10	1149.8	52.7	1524	4	US-09-688-489-109	Sequence 109, App
11	1149.8	52.7	1524	4	US-09-679-426-109	Sequence 109, App
12	1149.8	52.7	1524	4	US-09-759-143-109	Sequence 109, App
13	1149.8	52.7	1524	4	US-09-651-236-109	Sequence 109, App
14	1000.4	45.9	1297	2	US-08-727-688-9	Sequence 9, Appli
15	538.6	24.7	3498	4	US-09-949-016-1003	Sequence 1003, Ap
16	535.4	24.6	3498	4	US-09-949-016-5521	Sequence 5521, Ap
17	358	16.4	384	3	US-09-030-607-185	Sequence 185, App
18	358	16.4	384	3	US-09-439-313-185	Sequence 185, App
19	358	16.4	384	3	US-09-352-616A-185	Sequence 185, App
20	358	16.4	384	3	US-09-232-149A-185	Sequence 185, App
21	358	16.4	384	4	US-09-159-812-185	Sequence 185, App
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25	358	16.4	384	4	US-09-688-489-185	Sequence 185, App
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32	348.6	16.0	380	3	US-09-352-616A-84	Sequence 84, Appl
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44	257.2	11.8	6220	4	US-09-949-016-470	Sequence 470, App
45	255.6	11.7	6221	4	US-09-949-016-5229	Sequence 5229, Ap

ALIGNMENTS

RESULT 1
US-09-020-956-109
; Sequence 109, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1524 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-020-956-109

Query Match 52.7%; Score 1149.8; DB 3; Length 1524;
Best Local Similarity 88.6%; Pred. No. 1.8e-260;
Matches 1325; Conservative 3; Mismatches 0; Indels 167; Gaps 1;

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Qy      1513 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 1572
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Qy      1753 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTG 1812
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RESULT 2
US-09-030-607-109
; Sequence 109, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1524 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-607-109

Query Match 52.7%; Score 1149.8; DB 3; Length 1524;
Best Local Similarity 88.6%; Pred. No. 1.8e-260;
Matches 1325; Conservative 3; Mismatches 0; Indels 167; Gaps 1;

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Db      1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

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Qy      1916 ------------------------------------------------------------ 1915

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Db      1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

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Db      1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 1504
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RESULT 3
US-09-439-313-109
; Sequence 109, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-109

Query Match 52.7%; Score 1149.8; DB 3; Length 1524;
Best Local Similarity 88.6%; Pred. No. 1.8e-260;
Matches 1325; Conservative 3; Mismatches 0; Indels 167; Gaps 1;

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Qy       853 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 912
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Db        70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       973 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 1032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy      1033 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 1092
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Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       1093 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 1152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       1153 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 1212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       1213 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 1272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       1273 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 1332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       1333 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 1392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       1393 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 1452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       1453 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 1512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       1513 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 1572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       1573 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 1632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       1633 CTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 1692
             |||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       1693 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 1752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       1753 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTG 1812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       1813 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       1873 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------- 1915
             ||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       1916 ------------------------------------------------------------ 1915

Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       1916 ------------------------------------------------------------ 1915

Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       1916 ----------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1945
                                          |||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       1946 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 2005
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       2006 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 2065
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       2066 CCTGGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 2125
             ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       2126 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 1504
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RESULT 4
US-09-352-616A-109
; Sequence 109, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-109

Query Match 52.7%; Score 1149.8; DB 3; Length 1524;
Best Local Similarity 88.6%; Pred. No. 1.8e-260;
Matches 1325; Conservative 3; Mismatches 0; Indels 167; Gaps 1;

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Qy        853 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy        913 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy        973 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       1033 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       1093 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       1153 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       1213 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       1273 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 1332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489
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Qy       1333 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 1392
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Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       1393 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 1452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       1453 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 1512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       1513 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 1572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       1573 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 1632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       1633 CTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 1692
             ||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       1693 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 1752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       1753 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTG 1812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       1813 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       1873 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------- 1915
             ||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       1916 ---------------------------------------------------------- 1915

Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       1916 ---------------------------------------------------------- 1915

Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       1916 ------------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1945
                                           ||||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       1946 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 2005
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       2006 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 2065
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       2066 CCTGGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 2125
             ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       2126 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 1504

RESULT 5
US-09-232-149A-109
; Sequence 109, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer Lynn
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
;  TITLE OF INVENTION:  CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.427C6
;  CURRENT APPLICATION NUMBER: US/09/232,149A
;  CURRENT FILING DATE:  1999-01-15
;  NUMBER OF SEQ ID NOS: 338
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-232-149A-109

  Query Match            52.7%;  Score 1149.8;  DB 3;  Length 1524;
  Best Local Similarity  88.6%;  Pred. No. 1.8e-260;
  Matches 1325;  Conservative    3;  Mismatches    0;  Indels  167;  Gaps    1;

Qy        853 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy        913 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy        973 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       1033 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       1093 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       1153 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       1213 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       1273 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 1332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       1333 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 1392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       1393 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 1452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       1453 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 1512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       1513 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 1572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       1573 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 1632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789
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Qy       1633 CTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 1692
             ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       1693 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 1752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       1753 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTG 1812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       1813 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       1873 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------- 1915
             ||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       1916 ------------------------------------------------------------ 1915

Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       1916 ------------------------------------------------------------ 1915

Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       1916 ------------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1945
                                           ||||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       1946 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 2005
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       2006 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 2065
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       2066 CCTGGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 2125
             |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       2126 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 1504
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RESULT 6
US-09-159-812-109
; Sequence 109, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-159-812-109

Query Match 52.7%; Score 1149.8; DB 4; Length 1524;
Best Local Similarity 88.6%; Pred. No. 1.8e-260;
Matches 1325; Conservative 3; Mismatches 0; Indels 167; Gaps 1;

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Qy        853 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy        913 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy        973 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       1033 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       1093 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       1153 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       1213 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       1273 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 1332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       1333 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 1392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       1393 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 1452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       1453 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 1512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       1513 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 1572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       1573 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 1632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       1633 CTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 1692
              |||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       1693 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 1752
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       1753 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTG 1812
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       1813 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1872
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       1873 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------- 1915
              ||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089
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```
Qy       1916 ------------------------------------------------------------ 1915

Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       1916 ------------------------------------------------------------ 1915

Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       1916 ------------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1945
                                            ||||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       1946 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 2005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       2006 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 2065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       2066 CCTGGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 2125
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       2126 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 1504


RESULT 7
US-09-636-215-109
; Sequence 109, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.42717C17
;  CURRENT APPLICATION NUMBER: US/09/636,215
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS:  852
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-636-215-109

  Query Match             52.7%;  Score 1149.8;  DB 4;  Length 1524;
  Best Local Similarity   88.6%;  Pred. No. 1.8e-260;
  Matches 1325;  Conservative    3;  Mismatches    0;  Indels  167;  Gaps    1;

Qy        853 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy        913 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy        973 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       1033 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       1093 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       1153 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       1213 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       1273 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 1332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       1333 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 1392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       1393 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 1452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       1453 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 1512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       1513 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 1572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       1573 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 1632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       1633 CTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 1692
              ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       1693 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 1752
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       1753 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTG 1812
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       1813 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1872
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       1873 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------- 1915
              ||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       1916 ------------------------------------------------------------ 1915

Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       1916 ------------------------------------------------------------ 1915
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Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       1916 ----------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1945
                                          |||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       1946 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 2005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       2006 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 2065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       2066 CCTGGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 2125
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       2126 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 1504


RESULT 8
US-09-685-166A-109
; Sequence 109, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C21
;  CURRENT APPLICATION NUMBER: US/09/685,166A
;  CURRENT FILING DATE:  2000-10-10
;  NUMBER OF SEQ ID NOS: 898
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-685-166A-109

  Query Match             52.7%;  Score 1149.8;  DB 4;  Length 1524;
  Best Local Similarity   88.6%;  Pred. No. 1.8e-260;
  Matches 1325;  Conservative    3;  Mismatches    0;  Indels  167;  Gaps    1;

Qy        853 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy        913 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy        973 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       1033 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       1093 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       1153 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       1213 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       1273 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 1332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       1333 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 1392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       1393 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 1452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       1453 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 1512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       1513 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 1572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       1573 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 1632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       1633 CTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 1692
              ||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       1693 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 1752
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       1753 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTG 1812
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       1813 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1872
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       1873 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------- 1915
              ||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       1916 ------------------------------------------------------------ 1915

Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       1916 ------------------------------------------------------------ 1915

Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       1916 ----------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1945
                                          |||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269
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Qy       1946 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 2005
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       2006 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 2065
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Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       2066 CCTGGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 2125
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Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       2126 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 1504


RESULT 9
US-09-115-453-109
; Sequence 109, Application US/09115453B
; Patent No. 6657056
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT: Dillon, Davin C.
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
;  TITLE OF INVENTION: METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.427C4
;  CURRENT APPLICATION NUMBER: US/09/115,453B
;  CURRENT FILING DATE: 1998-07-14
;  NUMBER OF SEQ ID NOS: 228
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-115-453-109

  Query Match             52.7%;  Score 1149.8;  DB 4;  Length 1524;
  Best Local Similarity   88.6%;  Pred. No. 1.8e-260;
  Matches 1325;  Conservative    3;  Mismatches    0;  Indels  167;  Gaps    1;

Qy        853 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy        913 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy        973 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 1032
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Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       1033 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       1093 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 1152
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Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       1153 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 1212
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Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       1213 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 1272
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Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       1273 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 1332
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Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       1333 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 1392
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Db         490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       1393 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 1452
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Db         550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       1453 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 1512
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Db         610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       1513 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 1572
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Db         670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       1573 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 1632
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Db         730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       1633 CTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 1692
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Db         790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       1693 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 1752
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       1753 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTG 1812
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Db         910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       1813 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1872
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Db         970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       1873 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------- 1915
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       1916 ---------------------------------------------------------- 1915

Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       1916 ---------------------------------------------------------- 1915

Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       1916 ----------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1945
                                          ||||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       1946 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 2005
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Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       2006 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 2065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

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              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       2126 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
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Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 1504


RESULT 10
US-09-688-489-109
; Sequence 109, Application US/09688489
; Patent No. 6664377
```

```
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer Lynn
;  TITLE OF INVENTION:  COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
;  TITLE OF INVENTION:  CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE:  210121.427D2
;  CURRENT APPLICATION NUMBER: US/09/688,489
;  CURRENT FILING DATE:  2000-10-13
;  NUMBER OF SEQ ID NOS:  338
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-688-489-109

  Query Match             52.7%;  Score 1149.8;  DB 4;  Length 1524;
  Best Local Similarity   88.6%;  Pred. No. 1.8e-260;
  Matches 1325;  Conservative    3;  Mismatches    0;  Indels  167;  Gaps    1;

Qy        853 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 912
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Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy        913 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 972
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Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy        973 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 1032
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Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       1033 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 1092
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Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       1093 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 1152
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Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       1153 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 1212
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Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       1213 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 1272
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Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       1273 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 1332
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Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       1333 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 1392
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Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       1393 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 1452
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Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

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Qy       1513 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 1572
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Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       1573 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 1632
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Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       1633 CTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 1692
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Db         790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       1693 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 1752
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       1753 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTG 1812
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db         910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       1813 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1872
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Db         970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       1873 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------------- 1915
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Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       1916 ------------------------------------------------------------ 1915

Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       1916 ------------------------------------------------------------ 1915

Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       1916 ------------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1945
                                           ||||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       1946 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 2005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

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Qy       2066 CCTGGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 2125
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Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       2126 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
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Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 1504


RESULT 11
US-09-679-426-109
; Sequence 109, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
```

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;  FILE REFERENCE:  210121.427C20
;  CURRENT APPLICATION NUMBER: US/09/679,426
;  CURRENT FILING DATE:  2000-10-02
;  NUMBER OF SEQ ID NOS:  895
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-679-426-109

  Query Match             52.7%;  Score 1149.8;  DB 4;  Length 1524;
  Best Local Similarity   88.6%;  Pred. No. 1.8e-260;
  Matches 1325;  Conservative    3;  Mismatches    0;  Indels  167;  Gaps    1;

Qy        853 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 912
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Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy        913 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 972
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Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy        973 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 1032
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Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       1033 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 1092
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Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       1093 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 1152
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Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       1153 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 1212
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Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       1213 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 1272
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Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

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Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       1393 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 1452
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Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

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Qy       1573 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 1632
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Qy       1633 CTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 1692
              ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       1693 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 1752
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Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       1753 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTG 1812
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       1813 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1872
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       1873 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------- 1915
              ||||||||||||||||||||||||||||||||||||||||||
Db        1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       1916 ------------------------------------------------------------ 1915

Db        1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       1916 ------------------------------------------------------------ 1915

Db        1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       1916 ------------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1945
                                           ||||||||||||||||||||||||||||||
Db        1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       1946 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 2005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       2006 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 2065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       2066 CCTGGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 2125
              ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       2126 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 1504


RESULT 12
US-09-759-143-109
; Sequence 109, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C23
;  CURRENT APPLICATION NUMBER: US/09/759,143
;  CURRENT FILING DATE:  2001-01-12
;  NUMBER OF SEQ ID NOS:  934
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
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;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-759-143-109

  Query Match            52.7%;  Score 1149.8;  DB 4;  Length 1524;
  Best Local Similarity  88.6%;  Pred. No. 1.8e-260;
  Matches 1325;  Conservative    3;  Mismatches    0;  Indels  167;  Gaps    1;

Qy        853 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy        913 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy        973 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       1033 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       1093 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       1153 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       1213 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       1273 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 1332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       1333 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 1392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       1393 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 1452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       1453 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 1512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       1513 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 1572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       1573 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 1632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       1633 CTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 1692
              ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       1693 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 1752
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       1753 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTG 1812
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       1813 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1872
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       1873 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------- 1915
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       1916 ------------------------------------------------------------ 1915

Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       1916 ------------------------------------------------------------ 1915

Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       1916 ----------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1945
                                          ||||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       1946 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 2005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       2006 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 2065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       2066 CCTGGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 2125
              ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       2126 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 1504


RESULT 13
US-09-651-236-109
; Sequence 109, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.42718C18
;  CURRENT APPLICATION NUMBER: US/09/651,236
;  CURRENT FILING DATE:  2000-08-29
;  NUMBER OF SEQ ID NOS:  865
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-651-236-109

  Query Match            52.7%;  Score 1149.8;  DB 4;  Length 1524;
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  Best Local Similarity   88.6%;  Pred. No. 1.8e-260;
  Matches 1325;  Conservative    3;  Mismatches    0;  Indels  167;  Gaps    1;

Qy        853 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy        913 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy        973 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       1033 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       1093 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       1153 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       1213 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       1273 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 1332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       1333 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 1392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       1393 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 1452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       1453 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 1512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       1513 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 1572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       1573 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 1632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       1633 CTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 1692
              ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       1693 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 1752
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       1753 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTG 1812
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       1813 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1872
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       1873 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------- 1915
              ||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       1916 ---------------------------------------------------------- 1915

Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       1916 ---------------------------------------------------------- 1915

Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       1916 ----------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1945
                                           ||||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       1946 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 2005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       2006 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 2065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       2066 CCTGGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 2125
              ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       2126 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 1504


RESULT 14
US-08-727-688-9
; Sequence 9, Application US/08727688
; Patent No. 5919638
;  GENERAL INFORMATION:
;    APPLICANT:  Russell, John C.
;    TITLE OF INVENTION:  Reagents and Methods for Detecting Prostate Tumors
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Road D377/AP6D
;      CITY:  Abbott Park
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/727,688
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Porembski, Priscilla E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5967.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (847) 937-0378
;      TELEFAX:  (847) 938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1297 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-727-688-9
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  Query Match             45.9%;  Score 1000.4;  DB 2;  Length 1297;
  Best Local Similarity   97.9%;  Pred. No. 2.3e-225;
  Matches 1051;  Conservative    2;  Mismatches   16;  Indels    4;  Gaps    4;

Qy        854 TGCGCCAGGGCCTGAGCGGA-GGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 912
              |||||  | ||||||||||| || | | ||||||||||||||||||||||||||    ||
Db          1 TGCGCNGGAGCCTGAGCGGAGGGTGTGCGCAGCCTCGCCAGCGGGGGCCCCGGGCTGNGC 60

Qy        913 CA-TGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGA 971
              || |||||||||||||||||||||| |  ||||||||||||||||||||||||||||||
Db         61 CATTGCCTCACTGAGCCAGCGCCTGC-CTNCTACCTCGCCGACAGCTGGAACCAGTGCGA 119

Qy        972 CCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTA 1031
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 CCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTA 179

Qy       1032 CCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCA 1091
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCA 239

Qy       1092 CATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAA 1151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 CATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAA 299

Qy       1152 GGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCAC 1211
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Qy       1212 GGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTA 1271
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Qy       1272 CCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCAT 1331
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Qy       1332 GGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGC 1391
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Qy       1392 GGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCT 1451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1452 GCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGG 1511
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Qy       1512 CAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGA 1571
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        660 CAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAG-GTTACCGCCTCATCCGGGA 718

Qy       1572 ATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCT 1631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1632 GCTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCA 1691
              |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
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Qy       1692 TTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCA 1751
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Qy       1752 TAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCT 1811
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Qy       1812 GAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTA 1871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 GAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTA 1018

Qy       1872 CGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTACCTCGGCCC 1924
              |||||||||||||||||||||||||||||||||||||||||||||||||| |   | ||
Db       1019 CGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCC 1071


RESULT 15
US-09-949-016-1003
; Sequence 1003, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1003
;   LENGTH: 3498
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-1003

  Query Match             24.7%;  Score 538.6;  DB 4;  Length 3498;
  Best Local Similarity   58.6%;  Pred. No. 1.1e-116;
  Matches 1105;  Conservative    1;  Mismatches  680;  Indels   99;  Gaps    6;

Qy         35 AGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCA 94
              ||  ||||||| | |||||| | || |||||  || ||| |||| |      |||||||||
Db       1544 AGAACCCCTGGCGGGACCTGTTCCTGTGGGCCGTGCTGCAGAACCGCCACGAGATGGCCA 1603

Qy         95 TGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGC 154
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Qy        155 TCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGG 214
              ||   | |||| | | ||||||| | || || |||| |||    |   | |     | |
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Qy        215 CGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGG 274
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Qy        275 TGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCC 334
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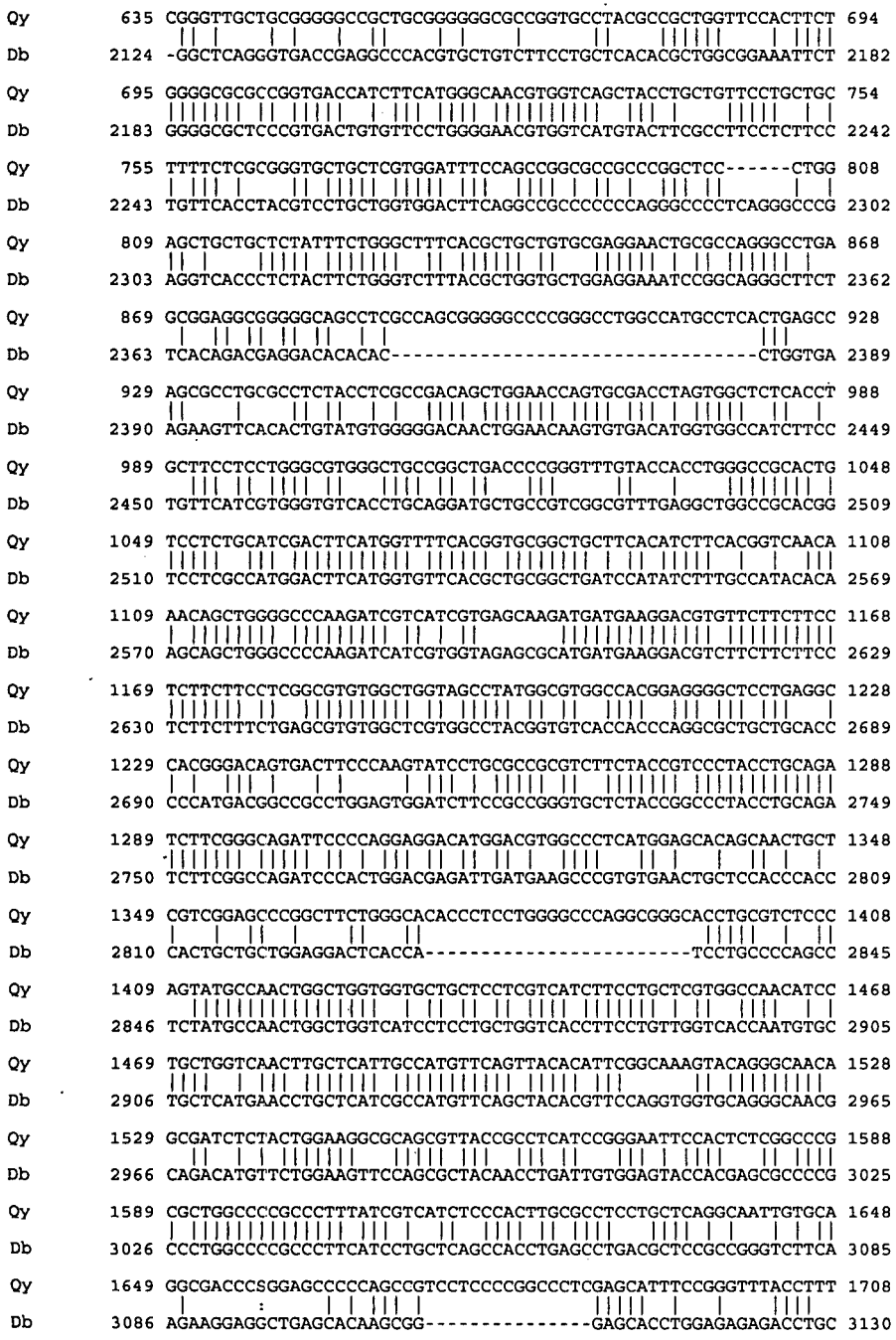
Qy        335 AGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGC 394
               | |||||||   | |||||||||   |||||||||||||| || || || ||| |  | |
Db       1838 ACCTGGCCACCGAGGCTGACGCCAAGGCCTTCTTTGCCCACGACGGCGTTCAGGCCTTCC 1897

Qy        395 TGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCG 454
              ||||   ||  |||||||| || ||||||      || ||||||  |   ||| |    |
Db       1898 TGACCAGGATCTGGTGGGGGGACATGGCCGCAGGCACGCCCATCCTGCGGCTGCTAGGAG 1957

Qy        455 CCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGG 514
              |||||  |||||  | ||| |||| |||  |||||||||||||||  |   ||
Db       1958 CCTTCCTCTGCCCCGCCCTCGTCTATACCAACCTCATCACCTTCAGTGAGGAAGCTCCCC 2017

Qy        515 AGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTG 574
               |   ||| |   ||||      |   ||| |||| ||  |     |  | | | ||
Db       2018 TGAGGACAGGCCTGGAGGACCTGCAGGACCTGGACAGCCTGGACACGGAGAAGAGCCCGC 2077

Qy        575 TCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTC 634
              |          | |       | | ||  || | ||| ||  ||| |
Db       2078 TGTATGGCCTGCAGAGCCGGGTGGAGGAGCTGGTGGAGGCGCCGAG-------------- 2123
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Search completed: June 13, 2005, 08:38:50
Job time : 256.801 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 16:55:33 ; Search time 4466.1 Seconds
(without alignments)
18579.996 Million cell updates/sec

Title: US-09-869-486B-25
Perfect score: 2180
Sequence: 1 tcgaggccaagaattcggca.....ggaaataaagccatttcaga 2180

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1088.2	49.9	4293	3	AK044094	AK044094 Mus muscu
2	770	35.3	912	6	CA488162	CA488162 AGENCOURT
3	719	33.0	879	5	BU858032	BU858032 AGENCOURT
4	651.6	29.9	883	5	BQ723742	BQ723742 AGENCOURT
5	647	29.7	864	6	CA488844	CA488844 AGENCOURT
6	634.4	29.1	672	4	BI759746	BI759746 603045620
7	609.8	28.0	613	5	BX474984	BX474984 DKFZp686M
8	579.8	26.6	599	4	BI910079	BI910079 603067915
9	577	26.5	580	5	BP265210	BP265210 BP265210
10	527	24.2	725	7	CK955668	CK955668 4095493 B
11	525.6	24.1	551	6	CB266373	CB266373 1005278 H
12	514.4	23.6	1090	2	BF311909	BF311909 601897749
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14	497.4	22.8	895	5	BQ918283	BQ918283 AGENCOURT
15	485.4	22.3	625	4	BI199159	BI199159 602758878
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17	465.6	21.4	3449	3	AK035197	AK035197 Mus muscu
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20	451	20.7	933	5	BQ942718	BQ942718 AGENCOURT
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22	447.4	20.5	624	7	CK832049	CK832049 4056009 B
23	443	20.3	444	4	BM821224	BM821224 K-EST0090
24	411.6	18.9	601	7	CO261067	CO261067 4133160 B
25	395	18.1	519	4	BI198633	BI198633 602761709
26	391.2	17.9	392	4	BM797899	BM797899 K-EST0081
27	389	17.8	569	7	CN677997	CN677997 E0104H02-
28	387.6	17.8	611	2	BE313619	BE313619 601153249
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30	382.8	17.6	869	4	BI488582	BI488582 603021110
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32	374.4	17.2	883	2	BF582966	BF582966 602097824
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34	370.2	17.0	774	4	BG759687	BG759687 602713380
c 35	368.8	16.9	734	6	CA312705	CA312705 UI-CF-FN0
c 36	367.8	16.9	733	5	BU687299	BU687299 UI-CF-EC1
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38	361.6	16.6	484	2	BF652205	BF652205 275703 MA
39	356	16.3	545	7	CO895866	CO895866 BovGen_24
40	352.6	16.2	676	7	CN790827	CN790827 4125460 B
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42	343	15.7	495	5	BQ371603	BQ371603 PM1-FN021
43	341.4	15.7	410	7	H18835	H18835 ym45d10.r1
44	341.2	15.7	432	2	BF041933	BF041933 BP250006A
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ALIGNMENTS

RESULT 1
AK044094
LOCUS AK044094 4293 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830089H13 product:similar to TRP-RELATED CATION INFLUX CHANNEL [Homo sapiens], full insert sequence.
ACCESSION AK044094
VERSION AK044094.1 GI:26336171
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 4293)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
FEATURES Location/Qualifiers
source 1. .4293
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/codon_start=1
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IREFHSRPALAPPLIIICHVSVSVRKQSGSC"
ORIGIN

Query Match 49.9%; Score 1088.2; DB 3; Length 4293;
Best Local Similarity 75.1%; Pred. No. 8.5e-236;

Matches 1426; Conservative 1; Mismatches 384; Indels 88; Gaps 2;

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Qy      26 GCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCAC 85
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Qy     146 GTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGA 205
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Qy     206 AAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCA 265
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Qy     266 GCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCA 325
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Qy     326 CTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTAC 385
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Qy     566 AAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGT 625
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Qy     626 CGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGT 685
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Qy     686 TCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGT 745
             |||||||||| || || |||||   |||| |||| || |||||||| ||||||||||
Db    1983 CGGACTTCTGGGGTGCCCCAGTGACTGCCTTCCTGGGTAATGTGGTCAGTTACCTGCTGT 2042

Qy     746 TCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCC 805
           |||||||||| ||  | |  ||| |||| |||||||||||||  |   |||  |   |
Db    2043 TCCTGCTGCTGTTTGCCCACGTGTTGCTGGTGGATTTCCAGCCCACAAAGCCAAGTGTCT 2102

Qy     806 TGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCC 865
             |||||||||| || |||||||| |||||| |||||||||||| ||||||||||||
Db    2103 CCGAGCTGCTGCTGTACTTCTGGGCCTTCACGTTGCTGTGCGAGGAGCTGCGCCAGGGCC 2162

Qy     866 TGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGA 925
           || | || ||| |||| ||||| ||||| ||||| |  || || | |   || | |||
Db    2163 TGGGTGGTGGCTGGGGTAGCCTGGCCAGTGGGGGACGTGGTCCGGACAGAGCTCCCCTGC 2222

Qy     926 GCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCA 985
           |||| || |||| |||||||||| | || | ||||||||| || |||||  |||| ||||
Db    2223 GCCATCGGCTGCACCTCTACCTCTCAGATACCTGGAACCAATGTGACCTGCTGGCACTCA 2282

Qy     986 CCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCA 1045
           |||||||||| |||||||| |||||||||||||||| || | |   || |||| ||||
Db    2283 CCTGCTTCCTGCTGGGCGTAGGCTGCCGGCTGACCCCTGGGCTCTTTGACTTGGGACGCA 2342

Qy    1046 CTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCA 1105
           | |||||||| | |||||||| | |||||  |||| ||||| |||||||||||||| |
Db    2343 CCGTCCTCTGCCTTGACTTCATGATCTTCACACTGCGCCTGCTGCACATCTTCACGGTGA 2402
```

```
Qy       1106 ACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCT 1165
             |||| |||||||||||||||| ||||| |||||||| |||||||||| || |||||||
Db       2403 ACAAGCAGCTGGGGCCCAAGATTGTCATAGTGAGCAAAATGATGAAGGATGTATTCTTCT 2462

Qy       1166 TCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGA 1225
             |||||||||||||| |||||||||| ||||| ||||| |||||||| |||||| ||||||
Db       2463 TCCTCTTCTTCCTCTGCGTGTGGCTTGTAGCTTATGGGGTGGCCACAGAGGGGATCCTGA 2522

Qy       1226 GGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGC 1285
             |||| | |||| |     | || |||||||||||| | |||||||||| || || ||||
Db       2523 GGCCCCAGGACCGCAGTCTACCGAGTATCCTGCGCAGGGTCTTCTACCGACCGTATCTGC 2582

Qy       1286 AGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACT 1345
             |||||||||| ||`|||||||||||||| |||||||||||||||||    |   | ||||
Db       2583 AGATCTTCGGACAAATTCCCCAGGAGGAAATGGACGTGGCCCTCATGATTCCAGGTAACT 2642

Qy       1346 GCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCT 1405
             ||||   |||||  |||| |||||| || ||    ||| ||   || ||| |||| || |
Db       2643 GCTCAATGGAGCGGGGCTCCTGGGCTCATCCGGAGGGGCCCGTCGCAGGCTCCTGTGTGT 2702

Qy       1406 CCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACA 1465
             |||||||||||||||||||||||||||| |||||||  || ||||| |||| |||||||| |
Db       2703 CCCAGTATGCCAACTGGCTGGTGGTGTTGCTCCTTATCGTCTTCTTGCTGGTGGCCAATA 2762

Qy       1466 TCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCA 1525
             ||||| || ||||| ||||||| |||||||||| ||||| ||| ||||||| || ||||
Db       2763 TCCTGTTGCTCAACCTGCTCATCGCCATGTTCAGCTACACCTTCAGCAAAGTGCACGGCA 2822

Qy       1526 ACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGC 1585
             ||||||| |||||||||||||| ||||| ||| |||||||||||||||||||| ||  |||
Db       2823 ACAGCGACCTCTACTGGAAGGCACAGCGCTACAGCCTCATCCGGGAATTCCATTCGAGGC 2882

Qy       1586 CCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGT 1645
             | || |||||||| ||| | ||| ||||||  ||
Db       2883 CTGCCCTGGCCCCACCCCTCATCATCATCTGTCA------------------------- 2916

Qy       1646 GCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACC 1705
                                                                | || | |
Db       2917 ----------------------------------------------------TGTGTCTGTC 2926

Qy       1706 TTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTC 1765
             | | |||||||| |||||||||||||| || ||||| || ||||| || |||||||| |
Db       2927 TCTGTAAGGAAGCAGAGCGGAAGCTGCTGACTTGGGAGTCTGTGCACAAAGAGAACTTCC 2986

Qy       1766 TGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAGCGCACGTCCC 1825
             || ||||||  ||| |||||||||| || || ||||| |||:|| |||| |||||||| |
Db       2987 TGTTGGCACAAGCTCGGGACAAGCGAGACAGTGACTCGGAGCGTTTGAAACGCACGTCTC 3046

Qy       1826 AGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGA 1885
             |||||||||||   |||||||| |||||||||| ||| | |||||||| | ||| ||||
Db       3047 AGAAGGTGGACACTGCACTGAAGCAGCTGGGACAGATCAGAGAGTACGATCGGCGTCTGA 3106

Qy       1886 AAGTGCTGGAGCGGGAGGTCCAGCAGTGTACCTCGGCCC 1924
                | ||||||| | |||||||| || ||| |    | ||
Db       3107 GGGGGCTGGAGAGAGAGGTCCAACACTGTTCTCGAGTCC 3145
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RESULT 2
CA488162
LOCUS CA488162 912 bp mRNA linear EST 14-NOV-2002
DEFINITION AGENCOURT_10808068 MAPcL Homo sapiens cDNA clone IMAGE:6719903 5', mRNA sequence.
ACCESSION CA488162
VERSION CA488162.1 GI:24949318
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 912)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14278 row: i column: 23
High quality sequence start: 28
High quality sequence stop: 728.
FEATURES Location/Qualifiers
source 1. .912
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6719903"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1, LNCaP"
/lab_host="EMDH10B"
/clone_lib="MAPcL"
/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."
ORIGIN

Query Match 35.3%; Score 770; DB 6; Length 912;
Best Local Similarity 98.8%; Pred. No. 1e-163;
Matches 773; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

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Qy       1146 GATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGT 1205
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         46 GATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGT 105

Qy       1206 GGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGT 1265
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGT 165

Qy       1266 CTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGC 1325
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGC 225

Qy       1326 CCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGC 1385
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 CCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGC 285

Qy       1386 CCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCAT 1445
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCAT 345

Qy       1446 CTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACAC 1505
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 CTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACAC 405

Qy       1506 ATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCAT 1565
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 ATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCAT 465

Qy       1566 CCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCG 1625
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 CCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCG 525

Qy       1626 CCTCCTGCTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCT 1685
             |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        526 CCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCT 585
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Qy       1686 CGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATC 1745
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 CGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATC 645

Qy       1746 GGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGA 1805
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 GGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGA 705

Qy       1806 GMGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCG 1865
             |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 GCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCG 765

Qy       1866 CGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTACCTCGGCCCC 1925
             ||||||||||||||||  ||||||||||||||||||||||||||||||  |||| |
Db        766 CGAGTACGAACAGCGCCCTGAAGTGCTGGAGCGGGAGGTCCAGCAGTGTACGCGGGCCTC 825

Qy       1926 CG 1927
              ||
Db        826 CG 827
```

RESULT 3
BU858032

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LOCUS       BU858032                879 bp    mRNA    linear   EST 16-OCT-2002
DEFINITION  AGENCOURT_10478874 NIH_MGC_107 Homo sapiens cDNA clone
            IMAGE:6647959 5', mRNA sequence.
ACCESSION   BU858032
VERSION     BU858032.1  GI:24043024
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 879)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2889  row: d  column: 07
            High quality sequence start: 11
            High quality sequence stop: 612.
FEATURES             Location/Qualifiers
     source          1. .879
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6647959"
                     /tissue_type="adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_107"
                     /note="Organ: breast; Vector: pOTB7; Site_1: EcoRI;
                     Site_2: XhoI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN
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  Query Match           33.0%;  Score 719;  DB 5;  Length 879;
  Best Local Similarity  96.6%;  Pred. No. 3.8e-152;
  Matches  799;  Conservative    0;  Mismatches   20;  Indels    8;  Gaps    6;

Qy        708 GACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGT 767
              ||||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACCATCTTCATGGGCTACCTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGT 60

Qy        768 GCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTG 827
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTG 120

Qy        828 GGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCT 887
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCT 180

Qy        888 CGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCT 947
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCT 240

Qy        948 CGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGG 1007
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGG 300

Qy       1008 CTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCAT 1067
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCAT 360

Qy       1068 GGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGAT 1127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGAT 420

Qy       1128 CGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTG 1187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTG 480

Qy       1188 GCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCC 1247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCC 540

Qy       1248 AAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCA 1307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCA 600

Qy       1308 GGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCC-GGCTTCT 1366
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        601 GGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGGCTTCT 660

Qy       1367 GGGCACACCCTCCTGGGG-CCCAGGCGGGCACCTGCG-TCTCCCAGTATGCCAACT-GGC 1423
              |||||||||||||||||| |||||  |||||||||||  |||||||||||||| ||| |||
Db        661 GGGCACACCCTCCTGGGGCCCCAGCGGGGCACCTGCGNTCTCCCAGTATGCCCACTGGGC 720

Qy       1424 TGGTGGTGCTGC-TCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTG 1482
              |||||||||||| ||| || |||||||||||||||||||||||||||||||||||||||||
Db        721 TGGTGGTGCTGCTTCCCCGCCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTG 780

Qy       1483 CTCATTGCCATGTTCAGTTACACA---TTCGGCAAAGTACAGGGCAA 1526
              |||||||||| |    |  |||   | || ||||||| |||| |
Db        781 CTCATTGCCAATGTTCAGTTAACACATTCCGCCAAAGTACCGGGCCA 827
```

RESULT 4
BQ723742

```
LOCUS       BQ723742                883 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8241174 Lupski_sympathetic_trunk Homo sapiens cDNA clone
            IMAGE:6186968 5', mRNA sequence.
ACCESSION   BQ723742
VERSION     BQ723742.1  GI:21862639
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 883)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

```
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13580  row: d  column: 09
            High quality sequence stop: 557.
FEATURES             Location/Qualifiers
     source          1. .883
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6186968"
                     /sex="male"
                     /tissue_type="sympathetic trunk"
                     /dev_stage="adult, 16 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_sympathetic_trunk"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.9 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine); available through Life
                     Technologies."
ORIGIN

  Query Match            29.9%;  Score 651.6;  DB 5;  Length 883;
  Best Local Similarity  94.3%;  Pred. No. 7.3e-137;
  Matches  709;  Conservative    0;  Mismatches   39;  Indels    4;  Gaps    3;

Qy        321 TGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGG 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGG 60

Qy        381 GGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTG 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTG 120

Qy        441 GGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACCTTCAG 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACCTTCAG 180

Qy        501 GAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAA 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAA 240

Qy        561 TGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCG 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCG 300

Qy        621 CCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCG 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCG 360

Qy        681 CTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCT 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCT 420

Qy        741 GCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGG 800
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Db        421 GCTGTTCTTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGG 480

Qy        801 CTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCA 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCA 540

Qy        861 GGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTC 920
              ||||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db        541 GGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCAGGTCTGGCCATGCCTC 600

Qy        921 A-CTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGG 979
              | ||||||||||||||||||||||||||||||||||||||||||||    |||| |||| ||
Db        601 ACCTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACAGCGGCGA-CTAGAGG 659

Qy        980 CTCTCACCTGCTTCCTCCTGGGC--GTGGGCTGCCGGCTGACCCCGGGTTTGTACCACCT 1037
              ||| |||||||||| ||||||||      |    |||  | |||||| | | || || |
Db        660 CTCCCACCTGCTTGCTCCTGGGCCGCGAGCTGCCCGCTTAACCCCGAGATCGTCCCCCTC 719

Qy       1038 GGGCCGCACTGTCCTCTGCATCGACTTCATGG 1069
              ||| | | |||  |||||||  ||  |   ||
Db        720 GGGACCCGCTGGGCTCTGCAAGGAAATTCGGG 751


RESULT 5
CA488844
LOCUS       CA488844                 864 bp    mRNA    linear   EST 14-NOV-2002
DEFINITION  AGENCOURT_10808212 MAPcL Homo sapiens cDNA clone IMAGE:6721042 5',
            mRNA sequence.
ACCESSION   CA488844
VERSION     CA488844.1  GI:24951635
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 864)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Kristi A. Egland, Ira Pastan
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14281  row: i  column: 10
            High quality sequence stop: 571.
FEATURES             Location/Qualifiers
     source          1. .864
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6721042"
                     /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
                     hTERT-HME1, LNCaP"
                     /lab_host="EMDH10B"
                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification:  26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee  & Ira Pastan:  Discovery of new breast
                     cancer genes encoding  membrane and secreted proteins.
                     Manuscript submitted."
ORIGIN

  Query Match            29.7%;  Score 647;  DB 6;  Length 864;
  Best Local Similarity  85.6%;  Pred. No. 8.1e-136;
  Matches  703;  Conservative    3;  Mismatches  114;  Indels    1;  Gaps    1;

Qy       1262 GCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACG 1321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACG 60

Qy       1322 TGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTG 1381
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Db         61 TGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTG 120

Qy       1382 GGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCG 1441
                                                                                                                    
Db        121 GGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCG 180

Qy       1442 TCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTT 1501
                                                                                                                    
Db        181 TCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTT 240

Qy       1502 ACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCC 1561
                                                                                                                    
Db        241 ACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCC 300

Qy       1562 TCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACT 1621
                                                                                                                    
Db        301 TCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACT 360

Qy       1622 TGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGG 1681
                                                                                                                    
Db        361 TGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGG 420

Qy       1682 CCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGG 1741
                                                                                                                    
Db        421 CCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGG 480

Qy       1742 AATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACT 1801
                                                                                                                    
Db        481 AATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACT 540

Qy       1802 CCGAGMGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACA 1861
                                                                                                                    
Db        541 CCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACA 600

Qy       1862 TCCGCGAGTACGAACAGCGCCTGAAAGTGCT-GGAGCGGGAGGTCCAGCAGTGTACCTCG 1920
                                                                                                                    
Db        601 TCCGCGAGTACGAACAGCGCCTGANAGTGCTGGGAGCGGGAGGTCCAGCAGTGTACGCGC 660

Qy       1921 GCCCCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTC 1980
                                                                                                                    
Db        661 TCCCCTGGGGGTTGNNNNNNNNNNNNNNCCNNNNNCNCCCCCNCCCCCNNCNCCNCCCCC 720

Qy       1981 AGGACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAAC 2040
                                                                                                                    
Db        721 GCGGGGGGGCCGCCCCCCGCCCCGCGGCCCCGCGCCGGGCCCCNCGCCGCCNCCGGNCCC 780

Qy       2041 CAGTCCCAGCCTGGGAGGATCAAGGCCTGGATCCCRGGCCG 2081
                                                                                                                    
Db        781 CCCCCNNCGCGCGGGNGCGCCNNGCCGCGGGCGNNGGGGCG 821


RESULT 6
BI759746
LOCUS       BI759746                672 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603045620F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185949 5',
            mRNA sequence.
ACCESSION   BI759746
VERSION     BI759746.1  GI:15751324
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 672)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11464  row: g  column: 06
            High quality sequence stop: 668.
FEATURES             Location/Qualifiers
     source          1. .672
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5185949"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_116"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female.  Library is
                     oligo-dT primed and  directionally cloned (EcoRV site is
                     destroyed upon cloning).  Average insert size 1.4 kb,
                     insert size range 1-3 kb.  Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber  (Invitrogen).  Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           29.1%;  Score 634.4;  DB 4;  Length 672;
  Best Local Similarity   99.4%;  Pred. No. 5.6e-133;
  Matches  668;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    3;

Qy        706 GTGACCATCTTCATGGGCAACGTGGTCA-GCTACCTGCTGTTCCTGCTGCTTTTCTCGCG 764
                                                                                                                    
Db          1 GTGACCATCTTCATGGGCAACGTGGTCACGCTACCTGCTGTTCCTGCTGCTTTTCTCGCG 60

Qy        765 GGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTT 824
                                                                                                                    
Db         61 GGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTT 120

Qy        825 CTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAG 884
                                                                                                                    
Db        121 CTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCA-GGCCTGAGCGGAGGCGGGGGCAG 179

Qy        885 CCTCGCCAGCGGGGGCCCC-GGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCT 943
                                                                                                                    
Db        180 CCTCGCCAGCGGGGGCCCCTGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCT 239

Qy        944 ACCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCG 1003
                                                                                                                    
Db        240 ACCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCG 299

Qy       1004 TGGGCTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACT 1063
                                                                                                                    
Db        300 TGGGCTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACT 359

Qy       1064 TCATGGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCA 1123
                                                                                                                    
Db        360 TCATGGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCA 419

Qy       1124 AGATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCG 1183
                                                                                                                    
Db        420 AGATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCG 479

Qy       1184 TGTGGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACT 1243
                                                                                                                    
Db        480 TGTGGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACT 539

Qy       1244 TCCCAAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTC 1303
                                                                                                                    
Db        540 TCCCAAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTC 599

Qy       1304 CCCAGGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCT 1363
                                                                                                                    
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Db        600 CCCAGGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCT 659

Qy       1364 TCTGGGCACACC 1375
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Db        660 TCTGGGCACAAC 671


RESULT 7
BX474984
LOCUS       BX474984               613 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp686M22173_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686M22173 5', mRNA sequence.
ACCESSION   BX474984
VERSION     BX474984.1  GI:31669181
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 613)
  AUTHORS   Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     EST (Bahr,A., Lauber,J., Mewes,H.W., Weil,B., et al.)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686M22173) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .613
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686M22173"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="686 (synonym: hlcc3)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

  Query Match            28.0%;  Score 609.8;  DB 5;  Length 613;
  Best Local Similarity  99.7%;  Pred. No. 2.1e-127;
  Matches  611;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        896 GGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACA 955
              |||| ||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db          1 GGGGGCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCTCCTCTACCTCGCCGACA 60

Qy        956 GCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGC 1015
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGC 120

Qy       1016 TGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCA 1075
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCA 180

Qy       1076 CGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCG 1135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCG 240

Qy       1136 TGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAG 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAG 300

Qy       1196 CCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCC 1255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCC 360

Qy       1256 TGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACA 1315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACA 420

Qy       1316 TGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACC 1375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACC 480

Qy       1376 CTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGC 1435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGC 540

Qy       1436 TCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGT 1495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGT 600

Qy       1496 TCAGTTACACATT 1508
              |||||||||||||
Db        601 TCAGTTACACATT 613


RESULT 8
BI910079
LOCUS       BI910079               599 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603067915F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217194 5',
            mRNA sequence.
ACCESSION   BI910079
VERSION     BI910079.1  GI:16173416
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 599)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11545  row: m  column: 03
            High quality sequence stop: 589.
FEATURES             Location/Qualifiers
     source          1. .599
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5217194"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_118"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match            26.6%;  Score 579.8;  DB 4;  Length 599;
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  Best Local Similarity   99.2%;  Pred. No. 1.3e-120;
  Matches  592;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy       1187 GGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCC 1246
             ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db          1 GGCTGGTAGCCTATGGCGTGG-CACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCC 59

Qy       1247 CAAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCC 1306
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 CAAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCC 119

Qy       1307 AGGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCT 1366
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 AGGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCT 179

Qy       1367 GGGCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGG 1426
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 GGGCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGG 239

Qy       1427 TGGTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCA 1486
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 TGGTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCA 299

Qy       1487 TTGCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGG 1546
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 TTGCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGG 359

Qy       1547 CGCAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTA 1606
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 CGCAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTA 419

Qy       1607 TCGTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCC 1666
             ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db        420 TCGTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCC 479

Qy       1667 AGCCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGA 1726
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 AGCCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGA 539

Qy       1727 AGCTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGG 1783
             |||||||||||||||||||||||||||||||||||||||||||||||||||||   ||
Db        540 AGCTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCCTAGG 596


RESULT 9
BP265210
LOCUS       BP265210                 580 bp    mRNA    linear   EST 16-SEP-2004
DEFINITION  BP265210 Sugano cDNA library, thyroid JTH Homo sapiens cDNA clone
            JTH00250, mRNA sequence.
ACCESSION   BP265210
VERSION     BP265210.1  GI:52180441
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 580)
  AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  TITLE     Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
  JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .580
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="JTH00250"
                     /tissue_type="thyroid"
                     /cell_line="JTH"
                     /clone_lib="Sugano cDNA library, thyroid JTH"
                     /note="thyroid tumor"
ORIGIN

  Query Match             26.5%;  Score 577;  DB 5;  Length 580;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-120;
  Matches  577;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        684 GTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCTGCT 743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCTGCT 63

Qy        744 GTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTC 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTC 123

Qy        804 CCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 CCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGG 183

Qy        864 CCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACT 923
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACT 243

Qy        924 GAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCT 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCT 303

Qy        984 CACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCG 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 CACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCG 363

Qy       1044 CACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGT 423

Qy       1104 CAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTT 1163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 CAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTT 483

Qy       1164 CTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCT 1223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCT 543

Qy       1224 GAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGC 1260
              |||||||||||||||||||||||||||||||||||||
Db        544 GAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGC 580


RESULT 10
CK955668
LOCUS       CK955668                 725 bp    mRNA    linear   EST 15-MAR-2004
DEFINITION  4095493 BARC 10BOV Bos taurus cDNA clone 10BOV34_D12 5', mRNA
            sequence.
ACCESSION   CK955668
VERSION     CK955668.1  GI:45470048
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 725)
  AUTHORS   Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay,
            G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
  TITLE     Production of EST from cDNA libraries derived from immunologically
            activated bovine gut
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Tad S. Sonstegard
            Bovine Functional Genomics Laboratory
            Animal and Natural Resources Institute
```

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           Bdlg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
           Tel: 3015048416
           Fax: 3015048414
           Email: tads@anri.barc.usda.gov
           Single pass sequencing. Bases called and trimmed with phred
           0.000925 using options -trim_alt " -trim_fasta. Vector identified
           by cross_match using options -minmatch 12 -minscore 12
           Plate: 34  row: D  column: 12
           Seq primer: CCCAGTCACGACGTTGTAAAACG
           High quality sequence stop: 725.
FEATURES             Location/Qualifiers
     source          1. .725
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="10BOV34_D12"
                     /sex="Male"
                     /tissue_type="Pooled"
                     /dev_stage="Multiple"
                     /lab_host="DH10B T1 phage resistant"
                     /clone_lib="BARC 10BOV"
                     /note="Organ: Small Intestine; Vector: pAgen-1; Site_1:
                     EcoRV; Site_2: NotI; Equimolar amounts of mRNA extracted
                     from proximal jejunums of 18 and 21 wk old steers, and
                     distal ileums of 14 day old calves. proximal jejunum
                     exposed to C. oncophora for 3 and 6 weeks, and distal
                     ileum exposed to C. parvum for 7 days"
ORIGIN

  Query Match           24.2%;  Score 527;  DB 7;  Length 725;
  Best Local Similarity   84.0%;  Pred. No. 1.3e-108;
  Matches  609;  Conservative    0;  Mismatches  110;  Indels    6;  Gaps    1;

Qy        863 GCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTG------GCCATG 916
              ||||| || | |||  ||||||||| ||||  ||||| |||||| | |       ||  |
Db          1 GCCTGGGCAGCGGCCTGGGCAGCCTGGCCATGGGGGGACCCGGGACAGACTCCCACCGGG 60

Qy        917 CCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTAG 976
              || ||||| |||  || ||||  ||||||||| | |||  ||||||||||||||||||| |
Db         61 CCCCACTGCGCCGTCGTCTGCAACTCTACCTCTCTGACGCCTGGAACCAGTGCGACCTGG 120

Qy        977 TGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCACC 1036
              |||| ||| |||||||| | ||||||||||||||| ||||||||||||  ||||  |||
Db        121 TGGCCCTCGCCTGCTTCGTTCTGGGCGTGGGCTGCAGGCTGACCCCGGGCCTGTATGACC 180

Qy       1037 TGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATCT 1096
              |||||||||||||||||| | ||||||||| | |||||| || ||||||| |||||||
Db        181 TGGGCCGCACTGTCCTCTGCCTTGACTTCATGATCTTCACGCTGAGGCTGCTGCACATCT 240

Qy       1097 TCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGACG 1156
              |||| ||||||||||||||||||||||||||||||||||||||||||| ||||||| |
Db        241 TCACAGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGGTGAAGGATG 300

Qy       1157 TGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAGG 1216
              |||||||||||||||||||||||||||||||||||||| ||||| || |||||||| ||||
Db        301 TGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTTGCCTACGGGGTGGCCACTGAGG 360

Qy       1217 GGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGTC 1276
              ||||||| ||||| | |||| ||  | |||| | |||||||||||| |||||||||| |
Db        361 GGCTCCTTAGGCCCCAGGACCGTAGCCTCCCGAATATCCTGCGCCGTGTCTTCTACCGGC 420

Qy       1277 CCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAGC 1336
              |||||||||||||||| |||||||| || |||| ||| ||||||||||||||||||||||
Db        421 CCTACCTGCAGATCTTTGGGCAGATCCCTCAGGGGGAGATGGACGTGGCCCTCATGGAGC 480

Qy       1337 ACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGCA 1396
              || ||||||| ||   || ||  ||||  ||||  |||||    |||  ||   | ||||
Db        481 ACGGCAACTGTTCACTGGGGCAGGGCTCATGGGGGCACCCCGAAGGGAACCTCTCTGGCA 540

Qy       1397 CCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTCG 1456
                |||||||| |  |||||||||||||||||||||| ||||| ||  ||||||||| |
Db        541 AATGCGTCTCGCTTTATGCCAACTGGCTGGTGGTGCTCCTCCTTGTTGTCTTCCTGCTGG 600

Qy       1457 TGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAAG 1516
              |||||||||||||||| ||||  |||||||||| ||||||||  | || ||||||||||
Db         601 TGGCCAACATCCTGCTGCTCAATCTGCTCATTGCGATGTTCAGCCATACCTTCGGCAAAG 660

Qy       1517 TACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTCC 1576
              | |||||||||||||| |||||||||||||||||||| ||| ||||||||||||||| |
Db         661 TGCAGGGCAACAGCGACCTCTACTGGAAGGCGCAGCGCTACAGCCTCATCCGGGAATTTC 720

Qy       1577 ACTCT 1581
              |||||
Db         721 ACTCT 725


RESULT 11
CB266373
LOCUS       CB266373                551 bp    mRNA    linear   EST 20-FEB-2003
DEFINITION  1005278 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens
            cDNA 5', mRNA sequence.
ACCESSION   CB266373
VERSION     CB266373.1  GI:28440959
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 551)
  AUTHORS   Yang,R.-Z., Shuldiner,A. and Gong,D.-W.
  TITLE     EST analysis of human adipose gene expression
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Gong Da-Wei
            Division of Endocrinology, Diabetes and Nutrition
            University of Maryland
            660 Redwood St, HH497, Baltimore, MD 21201, USA
            Tel: 410 706 1672
            Fax: 410 706 1622
            Email: dgong@medicine.umaryland.edu
            PCR PRimers
            FORWARD: CTCGGGAAGCGCGCCATTGTGTTGGT
            BACKWARD: AATACGACTCACTATAGGGCGAATTGG
            Seq primer: GTTGGTACCCGGGAATTC.
FEATURES             Location/Qualifiers
     source          1. .551
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /sex="Male and Female"
                     /tissue_type="Adipose"
                     /clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
                     /note="Vector: lambdaTriplEx"
ORIGIN

  Query Match           24.1%;  Score 525.6;  DB 6;  Length 551;
  Best Local Similarity   98.9%;  Pred. No. 2.6e-108;
  Matches  547;  Conservative    1;  Mismatches    3;  Indels    2;  Gaps    2;

Qy       1249 AGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAG 1308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAG 60

Qy       1309 GAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGG 1368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGG 120

Qy       1369 GCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTG 1428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTG 180

Qy       1429 GTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATT 1488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATT 240

Qy       1489 GCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCG 1548
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCG 300

Qy       1549 CAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATC 1608
                ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        301 CAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCG-CCTTTATC 359

Qy       1609 GTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAG 1668
                ||||||||||||||||||||||||||||||||||||||||| ||||||:||||||||||
Db        360 GTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCANGCGACCCCGGAGCCCCCAN 419

Qy       1669 CCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAG 1728
                |||| |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 CCGTNCTCCCCGG-CCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAG 478

Qy       1729 CTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAG 1788
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 CTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAG 538

Qy       1789 CGGGAGAGCGACT 1801
                |||||||||||||
Db        539 CGGGAGAGCGACT 551
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RESULT 12
BF311909

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LOCUS       BF311909               1090 bp    mRNA    linear   EST 21-NOV-2000
DEFINITION  601897749F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126764 5',
            mRNA sequence.
ACCESSION   BF311909
VERSION     BF311909.1  GI:11259680
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1090)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM1017  row: b  column: 13
            High quality sequence stop: 633.
FEATURES             Location/Qualifiers
     source          1. .1090
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4126764"
                     /tissue_type="neuroblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_19"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and  Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN
```

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  Query Match             23.6%;  Score 514.4;  DB 2;  Length 1090;
  Best Local Similarity   87.3%;  Pred. No. 1e-105;
  Matches  637;  Conservative    0;  Mismatches   76;  Indels   17;  Gaps    6;

Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
              | | | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 176

Qy         76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 236

Qy        136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 296

Qy        196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 356

Qy        256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 416

Qy        316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 476

Qy        376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 536

Qy        436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 596

Qy        496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTA--GAGTTTGACATGGATA--- 550
              |||||||||||||||||||| |||||||||||||||||    |||||||||||| |
Db        597 TTCAGGAAATCAGAAGAGGAG-CCACACGGGAGGAGCTAAGAGGTTTGACATGGACATAG 655

Qy        551 -GTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGA---CCCAGCCGAGAAGACGCCG 606
               ||      |  || |||||| ||||| ||   | |||   |    |   |||||| ||||
Db        656 GGTCATTACATGGGCGAAGGGGCTGTCCGGGACGGGGAGACCAAGCCGAGGAAGAAGCCG 715

Qy        607 CTGGGGGTCCCGCG-----CCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCC--GCTGCGG 659
              ||||||||||||||           || | |  ||||  ||   |||||||  ||   |
Db        716 CTGGGGGTCCCGCGGGCCAAACCGGGGCCGGCACGGGACGCATGGGGGGCCGAGCCAGGA 775

Qy        660 GGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCAT 719
              |||   |||| ||| | ||||   |   ||| |||| || ||||  ||   |  | ||
Db        776 GGGCGCCCGGGGCCAAAGCCGGATGGGTCACATCTGAGGGGCGCACGTTGACCACCTCCG 835

Qy        720 GGGCAACGTG 729
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Db        836 GGGCAACGGG 845
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RESULT 13
CN335029

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LOCUS       CN335029                540 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000427738180 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN335029
VERSION     CN335029.1  GI:47334963
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
```

```
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 540   Std Error: 0.00.
FEATURES              Location/Qualifiers
     source           1. .540
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /tissue_type="embryonic stem cells, embryoid bodies
                      derived from H1, H7 and H9 cells"
                      /clone_lib="GRN_EB"
                      /note="oligo dT primed, full-length enriched cDNA library
                      from embryoid body outgrowths derived from hES cell lines
                      H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                      conditions."
ORIGIN

  Query Match             22.9%;  Score 499.2;  DB 7;  Length 540;
  Best Local Similarity   98.9%;  Pred. No. 2.5e-102;
  Matches  524;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    2;

Qy        517 CCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTC 576
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 CGCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTC 70

Qy        577 GGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTCCC--GCGCCAGTCGGGCCGTC 634
              |||||||||||||||||||||||||||||||||||||||||    |||||||||||||||
Db         71 GGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCTGCAGCCAGTCGGGCCGTC 130

Qy        635 CGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCT 694
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 CGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCT 190

Qy        695 GGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGC 754
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGC 250

Qy        755 TTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGC 814
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 TTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGC 310

Qy        815 TGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAG 874
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 TGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAG 370

Qy        875 GCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCC 934
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 GCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCC 430

Qy        935 TGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCC 994
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 TGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCC 490

Qy        995 TCCTGGGCGTGGGCTGCCGGCTGACCCC-GGGTTTGTACCACCTGGGCCG 1043
              |||||||||||||||||||||||||||| ||||||||||||||||||||
Db        491 TCCTGGGCGTGGGCTGCCGGCTGACCCCGGGGTTTGTACCACCTGGGCCG 540


RESULT 14
BQ918283
LOCUS       BQ918283                 895 bp    mRNA    linear   EST 20-AUG-2002
DEFINITION  AGENCOURT_8880984 NCI_CGAP_Co24 Mus musculus cDNA clone
            IMAGE:6396337 5', mRNA sequence.
ACCESSION   BQ918283
VERSION     BQ918283.1  GI:22332981
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 895)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13892  row: h  column: 02
            High quality sequence stop: 641.
FEATURES              Location/Qualifiers
     source           1. .895
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="FVB/N"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:6396337"
                      /lab_host="DH10B (T1 phage-resistant)"
                      /clone_lib="NCI_CGAP_Co24"
                      /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.6 kb. Constructed by Life
                      Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             22.8%;  Score 497.4;  DB 5;  Length 895;
  Best Local Similarity   73.6%;  Pred. No. 7.1e-102;
  Matches  666;  Conservative    0;  Mismatches  226;  Indels   13;  Gaps    2;

Qy        478 TACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAG 537
              ||||||  ||| |||  ||||||||| |||||  |||||||||||| | |||| || ||
Db          1 TACACCAACCTTATCGTCTTCAGGAAGTCAGAGGAGGAGCCCACACAGAAGGATCTTGAC 60

Qy        538 TTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAG 597
              |||||  |||||  ||   ||| |||||  | |||  |||   |||||  |  || ||  | |
Db         61 TTTGATATGGACAGCAGCATCAATGGAGCAGGTCCTCCTGGGACTGTAGAACCCTCTGCA 120

Qy        598 AAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGC 657
              |||  | | ||  |              ||  | | |  | | |  |    ||  |   | | |
Db        121 AAGGTGGCCCTTG------------AGAGGCGGCAGCGGCGACGGCCAGGACGTGCCCTC 168

Qy        658 GGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTC 717
              |  |  ||  || |       |||||||   |||||||||| || || |||||   ||||
Db        169 TGCTGTGGCAAGTTCTCCAAGCGCTGGTCGGACTTCTGGGGTGCCCCAGTGACTGCCTTC 228

Qy        718 ATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTG 777
              ||||  || ||||||||  ||||||||||||||||||||||  ||  |  |  ||| |||| |||
Db        229 CTGGGTAATGTGGTCAGTTACCTGCTGTTCCTGCTGCTGTTTGCCCACGTGTTGCTGGTG 288

Qy        778 GATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACG 837
              ||||||||||  |   |||  |   |   ||||||||||| || ||||||| ||||||
Db        289 GATTTCCAGCCCACAAAGCCAAGTGTCTCCGAGCTGCTGCTGTACTTCTGGGCCTTCACG 348

Qy        838 CTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGG 897
              ||||||||||||  |||||||||||||||  | ||  ||| |||| |||||  ||||| |||
Db        349 TTGCTGTGCGAGGAGCTGCGCCAGGGCCTGGGTGGTGGCTGGGGTAGCCTGGCCAGTGGG 408

Qy        898 GGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGC 957
              ||  |  ||  ||  | |   ||  | |||  |||| ||  |||| ||||||||||  | ||  | |
Db        409 GGACGTGGTCCGGACAGAGCTCCCCTGCGCCATCGGCTGCACCTCTACCTCTCAGATACC 468

Qy        958 TGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTG 1017
              ||||||||  ||  |||||   ||||  ||||||||||||||  ||||||||  ||||||||||||
Db        469 TGGAACCAATGTGACCTGCTGGCACTCACCTGCTTCCTGCTGGGCGTAGGCTGCCGGCTG 528

Qy       1018 ACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACG 1077
              |||||  ||  | |   ||  ||||  |||||  |||||||||  |  |||||||  |  |||||
Db        529 ACCCCTGGGCTCTTTGACTTGGGACGCACCGTCCTCTGCCTTGACTTCATGATCTTCACA 588
```

```
Qy       1078 GTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTG 1137
              |||| ||||| ||||||||||||||| ||||| |||||||||||||||||| ||||| |||
Db        589 CTGCGCCTGCTGCACATCTTCACGGTGAACAAGCAGCTGGGGCCCAAGATTGTCATAGTG 648

Qy       1138 AGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCC 1197
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Db        649 AGCAAAATGATGAAGGATGTATTCTTCTTCCTCTTCTTCCTCTGCGTGTGGCTTGTAGCT 708

Qy       1198 TATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTG 1257
              ||||| |||||||| |||||| |||||| ||| | |||| |     | || |||||||||
Db        709 TATGGGGTGGCCACAGAGGGGATCCTGAAGCCCCAGGACCGCAGTCTACCGAGTATCCTG 768

Qy       1258 CGCCGCGTCTTCTACCGTCCCTACCTGCAGATC-TTCGGGCAGATTCCCCAGGAGGACAT 1316
              ||| | |||| |||||   |  | ||||||||| ||||| ||  |||||||||||||| ||
Db        769 CGCAGGGTCTCCTACCCGACGAATCTGCAGATCTTTCGGACAATTTCCCCAGGAGGAAAT 828

Qy       1317 GGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCC 1376
              ||||| ||||||||||   |   | ||||||||   |||  | ||  ||   |  | | |
Db        829 GGACGGGGCCCTCATGATTCCAGGTAACTGCTCAATGGAAGCGGGGCTCCCTGGGCTCAT 888

Qy       1377 TCCTG 1381
              ||| |
Db        889 TCCGG 893


RESULT 15
BI199159
LOCUS       BI199159                625 bp    mRNA    linear   EST 10-JUL-2001
DEFINITION  602758878F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4894242 5',
            mRNA sequence.
ACCESSION   BI199159
VERSION     BI199159.1  GI:14654180
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 625)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM1777  row: l  column: 19
            High quality sequence stop: 618.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4894242"
                     /tissue_type="neuroblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_19"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and  Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           22.3%;  Score 485.4;  DB 4;  Length 625;
  Best Local Similarity  98.6%;  Pred. No. 3.5e-99;

  Matches  500;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
              | | | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 178

Qy         76 AACA-GGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGC 134
              |||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 AACATGGTCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGC 238

Qy        135 TCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGC 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 TCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGC 298

Qy        195 AGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGA 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 AGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGA 358

Qy        255 GTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTG 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        315 GGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCA 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 GGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCA 478

Qy        375 GGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACC 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 GGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACC 538

Qy        435 CATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCAC 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 CATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCAC 598

Qy        495 CTTCAGGAAATCAGAAGAGGAGCCCAC 521
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Db        599 CTTCAGGAAATCAGAAGAGGAGCCCAC 625


Search completed: June 13, 2005, 08:20:41
Job time : 4477.1 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 04:57:16 ; Search time 728.137 Seconds
(without alignments)
17723.358 Million cell updates/sec

Title: US-09-869-486B-25
Perfect score: 2180
Sequence: 1 tcgaggccaagaattcggca.....ggaaataaagccatttcaga 2180

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2178.8	99.9	2180	3	AAA49921	Aaa49921 Human cal
2	1978.8	90.8	3583	11	ADL33391	Adl33391 Human tra
3	1978.8	90.8	3676	12	ADQ83682	Adq83682 Human tum
4	1978.8	90.8	3676	13	ADQ85834	Adq85834 Human tum
5	1978.8	90.8	3676	13	ADQ86998	Adq86998 Human tum
6	1978.8	90.8	3900	5	AAH76383	Aah76383 Human TLC
7	1978.8	90.8	3900	8	ABS58041	Abs58041 Human tra
8	1978.8	90.8	3900	12	ADH51622	Adh51622 Human 186
9	1978.8	90.8	4061	3	AAA49923	Aaa49923 Human cal
10	1978.8	90.8	4061	10	ADH62711	Adh62711 Ca activa
11	1978.8	90.8	4061	13	ADR73511	Adr73511 Human TRP
12	1978.8	90.8	4061	13	ADS12774	Ads12774 Transient
13	1978.8	90.8	4641	11	ADN39239	Adn39239 Cancer/an
14	1977.2	90.7	2695	6	AAD32373	Aad32373 Human Trp
15	1977.2	90.7	4042	6	AAD32372	Aad32372 Human Trp
16	1975.6	90.6	3810	6	ABK92167	Abk92167 Prostate
17	1975.6	90.6	3810	13	ADR66772	Adr66772 Human pro
18	1975.6	90.6	3810	13	ADR65869	Adr65869 Human pro
19	1975.6	90.6	3810	13	ADS12778	Ads12778 Human TRP
20	1975.6	90.6	3898	12	ADL06463	Adl06463 Human tum
21	1974	90.6	3701	13	ADS12776	Ads12776 Transient
22	1968.2	90.3	3599	6	ABK28677	Abk28677 Human cDN
23	1943.8	89.2	2459	12	ADL06424	Adl06424 Human tum
24	1892.2	86.8	3387	5	AAH76384	Aah76384 Human TLC
25	1892.2	86.8	3390	12	ADH51624	Adh51624 Human 186
26	1892.2	86.8	3501	6	ABK92224	Abk92224 Prostate
27	1892.2	86.8	3501	11	ADN39597	Adn39597 Cancer/an
28	1891	86.7	2393	2	AAV26656	Aav26656 Human PS1
29	1891	86.7	2393	3	AAA64090	Aaa64090 Consensus
30	1202	55.1	2176	12	ADQ96621	Adq96621 Human PS1
31	1149.8	52.7	1524	2	AAV58585	Aav58585 Prostate
32	1149.8	52.7	1524	2	AAV61200	Aav61200 Full leng
33	1149.8	52.7	1524	3	AAA06348	Aaa06348 Human imm
34	1149.8	52.7	1524	3	ABS71253	Abs71253 Human pro
35	1149.8	52.7	1524	4	AAH93464	Aah93464 Human pro
36	1149.8	52.7	1524	4	AAS63556	Aas63556 Human pro
37	1149.8	52.7	1524	4	AAH02529	Aah02529 Prostate
38	1149.8	52.7	1524	4	AAH84778	Aah84778 Human pro
39	1149.8	52.7	1524	5	ACA59365	Aca59365 Prostate
40	1149.8	52.7	1524	5	AAS10107	Aas10107 Human pro
41	1149.8	52.7	1524	6	ABL94928	Abl94928 Human J1-
42	1149.8	52.7	1524	6	ABS58637	Abs58637 Prostate
43	1149.8	52.7	1524	8	ACC95092	Acc95092 Prostate
44	1149.8	52.7	1524	10	ADB13559	Adb13559 Human pro
45	1149.8	52.7	1524	10	ADG25975	Adg25975 Human pro

ALIGNMENTS

RESULT 1
AAA49921
ID AAA49921 standard; cDNA; 2180 BP.
XX
AC AAA49921;
XX
DT 10-OCT-2000 (first entry)
XX
DE Human calcium channel SOC-3/CRAC-2 partial cDNA.
XX
KW SOC-3/CRAC-2; calcium channel; human; store operated channel;
KW calcium release activated channel; therapy; diagnosis;
KW lymphocyte proliferative disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .2180
FT /*tag= a
FT /partial
XX
PN WO200040614-A2.
XX
PD 13-JUL-2000.
XX
PF 20-DEC-1999; 99WO-US029996.
XX
PR 30-DEC-1998; 98US-0114220P.
PR 29-JAN-1999; 99US-0120018P.
PR 22-JUN-1999; 99US-0140415P.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Scharenberg AM;
XX
DR WPI; 2000-465957/40.
DR P-PSDB; AAY95434.
XX
PT New SOC/CRAC calcium channel polynucleotides and polypeptides used to
PT diagnose and treat proliferative disorders associated with the channel,
PT and to screen for novel modulators of the channel.
XX
PS Claim 1(a); Page 90-91; 108pp; English.

XX
CC The present sequence is a partial nucleotide sequence of human SOC-3/CRAC
CC -2 cDNA. A partial open reading frame encodes the C-terminal portion (see
CC AAY95434) of SOC-3/CRAC-2, a member of a novel family of store operated
CC channel (SOC) or calcium release activated channel (CRAC) polypeptides
CC that modulate Ca2+ flux into and out of a cell, and which may be
CC activated upon depletion of Ca2+ from intracellular calcium stores,
CC allowing Ca2+ influx into a cell. SOC-3/CRAC-2 (full-length cDNA given in
CC AAA49923) is expressed predominantly in the kidney and colon.
CC Compositions for expressing SOC/CRAC calcium channel polypeptides in
CC cells may be useful for treating patients that have reduced extracellular
CC calcium influx into their SOC/CRAC-expressing cells. They will also be
CC useful for delivering therapeutic and/or imaging agents to such cells to
CC modulate proliferation and growth. SOC/CRAC polypeptides also represent
CC targets for designing and/or identifying inhibitors that block lymphocyte
CC proliferation and binding agents that selectively bind to SOC/CRAC
CC polypeptides to which drugs or toxins can be conjugated for delivery to
CC SOC/CRAC expressing cells. SOC/CRAC polynucleotides are used as probes
CC and primers to identify other members of the SOC/CRAC family of calcium
CC channels, as diagnostic reagents for identifying the presence of SOC/CRAC
CC polypeptides in biological samples, as agents for generating SOC/CRAC
CC binding polypeptides, and in gene therapy. Methods for determining the
CC level of SOC/CRAC expression in a subject can be used to assess the
CC presence, or absence, or stage of a proliferative disorder, e.g. a
CC lymphocyte proliferative disorder
XX
SQ Sequence 2180 BP; 365 A; 694 C; 667 G; 451 T; 0 U; 3 Other;

Query Match 99.9%; Score 2178.8; DB 3; Length 2180;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TCGAGGCCAAGAATTCGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTT 60
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Db          1 TCGAGGCCAAGAATTCGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTT 60

Qy         61 TGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 GCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCT 180
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Qy        181 GACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTT 240
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Qy        241 GACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGT 300
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Qy        301 CGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGT 360
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Db        301 CGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGT 360

Qy        361 GCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATG 420
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Db        361 GCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATG 420

Qy        421 GCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        481 ACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTT 540

Qy        541 GACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        601 ACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGG 660

Qy        661 GGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        721 GGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGAT 780

Qy        781 TTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTG 840

Qy        841 CTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGC 900

Qy        901 CCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGG 960

Qy        961 AACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACC 1020

Qy       1021 CCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTG 1080

Qy       1081 CGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGC 1140

Qy       1141 AAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTAT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTAT 1200

Qy       1201 GGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGC 1260

Qy       1261 CGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGAC 1320

Qy       1321 GTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCT 1380

Qy       1381 GGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTC 1440

Qy       1441 GTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGT 1500

Qy       1501 TACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGC 1560

Qy       1561 CTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCAC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCAC 1620

Qy       1621 TTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCG 1680

Qy       1681 GCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1681 GCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGG 1740

Qy       1741 GAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGAC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGAC 1800

Qy       1801 TCCGAGMGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACAC 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TCCGAGMGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACAC 1860

Qy       1861 ATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTACCTCG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 ATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTACCTCG 1920

Qy       1921 GCCCCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GCCCCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTC 1980

Qy       1981 AGGACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAAC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 AGGACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAAC 2040

Qy       2041 CAGTCCCAGCCTGGGAGGATCAAGGCCTGGATCCCRGGCCGTTATCCATCTGGAGGCTGC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CAGTCCCAGCCTGGGAGGATCAAGGCCTGGATCCCRGGCCGTTATCCATCTGGAGGCTGC 2100

Qy       2101 AGGGTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATTCCTCACACTGG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 AGGGTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATTCCTCACACTGG 2160

Qy       2161 GGAAATAAAGCCATTTCAGA 2180
             ||||||||||||||||||||
Db       2161 GGAAATAAAGCCATTTCAGA 2180
```

RESULT 2
ADL33391
ID ADL33391 standard; DNA; 3583 BP.
XX
AC ADL33391;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human transporter and ion channel (TRICH) gene #36.
XX
KW anti-HIV; antiallergic; antiinflammatory; antianemic; antiparkinsonian;
KW nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
KW antidiabetic; aephrotropic; antigout; thyromimetic; neuroprotective;
KW osteopathic; antiarthritic; antiparasitic; antihelmintic; antipsoriatic;
KW uropathic; ophthalmological; antirheumatic; hemostatic; antibacterial;
KW virucide; protozoacide; fungicide; gene therapy; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT allele replace(711,T)
FT /*tag= a
FT allele replace(1624,T)
FT /*tag= b
FT allele replace(1937,T)
FT /*tag= c
XX
PN WO2003083085-A2.
XX
PD 09-OCT-2003.
XX
PF 27-MAR-2003; 2003WO-US009797.
XX
PR 28-MAR-2002; 2002US-0368840P.
PR 26-APR-2002; 2002US-0375637P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Marquis JP, Lee SY, Emerling BM, Hafalia AJA, Khare R, Kable AE;
PI Richardson TW, Swarnakar A, Chawla NK, Becha SD, Mason PM;
PI Elliott VS, Ramkumar J, Griffin JA, Tran UK, Ison CH, Lindquist EA;
PI Jiang X, Jackson AA, Wilson AD, Jin P, Chang H;
XX
DR WPI; 2003-833535/77.
DR P-PSDB; ADL33332.
XX
PT New human transporters and ion channels (TRICH) and polynucleotides,
PT useful for diagnosing, treating or preventing autoimmune or inflammatory
PT disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, cancer or
PT hepatitis.
XX
PS Claim 12; SEQ ID NO 95; 405pp; English.
XX
CC The invention relates to an isolated polypeptide (I), which is a human
CC intracellular signaling molecule, which is a human intracellular
CC signaling molecule,a naturally occurring amino acid sequence at least 90%
CC -96% identical to it or a biologically active fragment or an immunogenic
CC fragment of the polypeptide. . The human TRICH, polynucleotides, agonists
CC and antagonists are useful for diagnosing, treating or preventing
CC disorders associated with aberrant expression of TRICH, particularly cell
CC proliferative disorders (e.g. arteriosclerosis, atherosclerosis,
CC cirrhosis, hepatitis, paroxysmal nocturnal hemoglobinuria, polycythemia
CC vera, psoriasis, primary thromobocytopenia or cancer), developmental
CC disorders (e.g. renal tubular acidosis, anemia or mental retardation),
CC neurological disorders (e.g. Alzheimers disease, Parkinson's disease or
CC epilepsy), autoimmune/inflammatory disorders (e.g. AIDS, allergies,
CC asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease,
CC diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout,
CC Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,
CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
CC bacterial, fungal, parasitic, protozoan or helminthic infections. The
CC polynucleotides encoding TRICH are useful for creating transgenic animals
CC to model human disease. This sequence corresponds to the gene encoding
CC one of the proteins of the invention.
XX
SQ Sequence 3583 BP; 633 A; 1119 C; 1124 G; 707 T; 0 U; 0 Other;

Query Match 90.8%; Score 1978.8; DB 11; Length 3583;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;

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Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
              | | | | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1205 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1264

Qy         76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1265 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 1324

Qy        136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1325 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 1384

Qy        196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1385 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1444

Qy        256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1445 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 1504

Qy        316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1505 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 1564

Qy        376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1565 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 1624
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Qy       436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
Db      1625 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 1684

Qy       496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555
Db      1685 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 1744

Qy       556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
Db      1745 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 1804

Qy       616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
Db      1805 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 1864

Qy       676 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 735
Db      1865 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 1924

Qy       736 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 795
Db      1925 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 1984

Qy       796 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 855
Db      1985 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 2044

Qy       856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
Db      2045 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 2104

Qy       916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
Db      2105 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 2164

Qy       976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035
Db      2165 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 2224

Qy      1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
Db      2225 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 2284

Qy      1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155
Db      2285 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 2344

Qy      1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215
Db      2345 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 2404

Qy      1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275
Db      2405 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 2464

Qy      1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335
Db      2465 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 2524

Qy      1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395
Db      2525 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 2584

Qy      1396 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 1455
Db      2585 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 2644

Qy      1456 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 1515
Db      2645 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 2704

Qy      1516 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 1575
Db      2705 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 2764

Qy      1576 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 1635
Db      2765 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 2824

Qy      1636 AGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 1695
Db      2825 AGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 2884

Qy      1696 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 1755
Db      2885 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 2944

Qy      1756 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG 1815
Db      2945 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAG 3004

Qy      1816 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 1875
Db      3005 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 3064

Qy      1876 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------- 1915
Db      3065 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTG 3124

Qy      1916 ---------- 1915
Db      3125 GCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTG 3184

Qy      1916 ---------- 1915
Db      3185 CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATT 3244

Qy      1916 ----------CCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 1948
Db      3245 TTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 3304

Qy      1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008
Db      3305 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 3364

Qy      2009 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 2068
Db      3365 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 3424

Qy      2069 GGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 2128
Db      3425 GGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 3484

Qy      2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
Db      3485 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 3536
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RESULT 3
ADQ83682
ID ADQ83682 standard; cDNA; 3676 BP.
XX
AC ADQ83682;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #496.
XX
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004060270-A2.
XX

PD 22-JUL-2004.
XX
PF 15-OCT-2003; 2003WO-US029126.
XX
PR 18-OCT-2002; 2002US-0418988P.
XX
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX
PI Wu TD, Zhou Y;
XX
DR WPI; 2004-534300/51.
XX
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
PS Claim 1; SEQ ID NO 496; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 3676 BP; 627 A; 1148 C; 1171 G; 730 T; 0 U; 0 Other;

Query Match 90.8%; Score 1978.8; DB 12; Length 3676;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;

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Qy        16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
             | | | | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1343 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1402

Qy        76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1403 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 1462

Qy       136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1463 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 1522

Qy       196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1523 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1582

Qy       256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1583 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 1642

Qy       316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1643 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 1702

Qy       376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1703 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 1762

Qy       436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1763 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 1822

Qy       496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1823 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 1882

Qy       556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1883 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 1942

Qy       616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1943 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGCGCCGGTGCCTA 2002

Qy       676 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2003 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 2062

Qy       736 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 795
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2063 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 2122

Qy       796 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 855
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2123 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 2182

Qy       856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2183 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 2242

Qy       916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2243 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 2302

Qy       976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2303 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 2362

Qy      1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2363 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 2422

Qy      1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2423 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 2482

Qy      1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2483 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 2542

Qy      1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2543 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 2602

Qy       1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2603 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 2662

Qy       1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2663 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 2722

Qy       1396 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 1455
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2723 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 2782

Qy       1456 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 1515
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2783 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 2842

Qy       1516 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 1575
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2843 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 2902

Qy       1576 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 1635
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2903 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 2962

Qy       1636 AGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 1695
             |||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db       2963 AGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 3022

Qy       1696 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 1755
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3023 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 3082

Qy       1756 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG 1815
             ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db       3083 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAG 3142

Qy       1816 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 1875
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3143 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 3202

Qy       1876 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------------- 1915
             ||||||||||||||||||||||||||||||||||||||||
Db       3203 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTG 3262

Qy       1916 ------------------------------------------------------------ 1915

Db       3263 GCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTG 3322

Qy       1916 ------------------------------------------------------------ 1915

Db       3323 CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATT 3382

Qy       1916 ----------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 1948
                                          ||||||||||||||||||||||||||||||||
Db       3383 TTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 3442

Qy       1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3443 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 3502

Qy       2009 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 2068
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3503 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 3562

Qy       2069 GGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 2128
             |||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3563 GGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 3622

Qy       2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3623 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 3674
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RESULT 4
ADQ85834
ID   ADQ85834 standard; cDNA; 3676 BP.
XX
AC   ADQ85834;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Human tumour-associated antigenic target (TAT) cDNA sequence #2703.
XX
KW   human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW   cancer; cell proliferative disorder; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004060270-A2.
XX
PD   22-JUL-2004.
XX
PF   15-OCT-2003; 2003WO-US029126.
XX
PR   18-OCT-2002; 2002US-0418988P.
XX
PA   (GETH ) GENENTECH INC.
PA   (WUTD/) WU T D.
PA   (ZHOU/) ZHOU Y.
XX
PI   Wu TD,  Zhou Y;
XX
DR   WPI; 2004-534300/51.
XX
PT   New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT   preventing or treating cell proliferative disorders such as cancer.
XX
PS   Claim 1; SEQ ID NO 2703; 5504pp; English.
XX
CC   The present invention describes an isolated tumour-associated antigenic
CC   target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC   sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC   (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC   sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC   (c). Also described: (1) an expression vector comprising the above
CC   nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC   a process for producing a polypeptide; (4) an isolated polypeptide
CC   comprising: (a) an amino acid sequence encoded by any of the above
CC   nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC   length coding region of the above nucleotide sequences; or (c) a sequence
CC   having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC   comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC   an isolated antibody that binds to the above polypeptide; (7) a process
CC   for producing the antibody; (8) an isolated oligopeptide that binds to
CC   the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC   binding organic molecule that binds to the above polypeptide; (10) a
CC   composition of matter comprising the above (chimeric) polypeptide,
CC   antibody, oligopeptide or TAT binding organic molecule, in combination
CC   with a carrier; (11) an article of manufacture comprising a container and
CC   the composition of matter contained within the container; (12) methods of
CC   inhibiting the growth of a cell that expresses the above protein, where
CC   the growth of the cell is at least in part dependent upon a growth
CC   potentiating effect of the above protein; (13) a method of
CC   therapeutically treating a mammal having a cancerous tumour comprising
CC   cells that express the above protein; (14) a method of determining the
CC   presence of a protein in a sample suspected of containing the protein
CC   described above; (15) methods of diagnosing the presence of a tumour in a
CC   mammal; (16) a method for treating or preventing a cell proliferative
CC   disorder associated with increased expression or activity of the above
CC   protein; and (17) a method of binding an antibody, oligopeptide or
CC   organic molecule to a cell that expresses the protein described above.
CC   The TAT sequences have cytostatic activities, and can be used in gene
CC   therapy. The composition and methods are useful for diagnosing,
CC   preventing or treating cancer. The composition is also used for preparing
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CC   a medicament for the therapeutic treatment or diagnostic detection of a
CC   cell proliferative disorder or cancer. The present sequence represents a
CC   human TAT cDNA sequence from the present invention.
XX
SQ   Sequence 3676 BP; 627 A; 1148 C; 1171 G; 730 T; 0 U; 0 Other;

  Query Match           90.8%;  Score 1978.8;  DB 13;  Length 3676;
  Best Local Similarity  92.5%;  Pred. No. 0;
  Matches 2157;  Conservative    3;  Mismatches    5;  Indels  167;  Gaps    1;

Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
Db       1343 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1402

Qy         76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
Db       1403 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 1462

Qy        136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
Db       1463 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 1522

Qy        196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
Db       1523 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1582

Qy        256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
Db       1583 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 1642

Qy        316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
Db       1643 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 1702

Qy        376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
Db       1703 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 1762

Qy        436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
Db       1763 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 1822

Qy        496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555
Db       1823 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 1882

Qy        556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
Db       1883 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 1942

Qy        616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
Db       1943 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 2002

Qy        676 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 735
Db       2003 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 2062

Qy        736 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 795
Db       2063 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 2122

Qy        796 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 855
Db       2123 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 2182

Qy        856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
Db       2183 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 2242

Qy        916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
Db       2243 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 2302

Qy        976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035
Db       2303 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 2362

Qy       1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
Db       2363 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 2422

Qy       1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155
Db       2423 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 2482

Qy       1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215
Db       2483 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 2542

Qy       1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275
Db       2543 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 2602

Qy       1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335
Db       2603 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 2662

Qy       1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395
Db       2663 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 2722

Qy       1396 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 1455
Db       2723 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 2782

Qy       1456 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 1515
Db       2783 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 2842

Qy       1516 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 1575
Db       2843 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 2902

Qy       1576 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 1635
Db       2903 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 2962

Qy       1636 AGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 1695
Db       2963 AGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 3022

Qy       1696 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 1755
Db       3023 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 3082

Qy       1756 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG 1815
Db       3083 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAG 3142

Qy       1816 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 1875
Db       3143 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 3202

Qy       1876 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------- 1915
Db       3203 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTG 3262

Qy       1916 ---------- 1915
Db       3263 GCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTG 3322

Qy       1916 ---------- 1915
Db       3323 CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATT 3382
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Qy       1916 ----------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 1948
                                          |||||||||||||||||||||||||||||||||
Db       3383 TTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 3442

Qy       1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3443 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 3502

Qy       2009 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 2068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3503 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 3562

Qy       2069 GGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 2128
              |||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3563 GGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 3622

Qy       2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3623 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 3674
```

RESULT 5
ADQ86998
ID ADQ86998 standard; cDNA; 3676 BP.
XX
AC ADQ86998;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3873.
XX
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004060270-A2.
XX
PD 22-JUL-2004.
XX
PF 15-OCT-2003; 2003WO-US029126.
XX
PR 18-OCT-2002; 2002US-0418988P.
XX
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX
PI Wu TD, Zhou Y;
XX
DR WPI; 2004-534300/51.
XX
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
PS Claim 1; SEQ ID NO 3873; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 3676 BP; 627 A; 1148 C; 1171 G; 730 T; 0 U; 0 Other;

Query Match 90.8%; Score 1978.8; DB 13; Length 3676;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;

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Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
              | | | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1343 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1402

Qy         76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1403 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 1462

Qy        136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1463 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 1522

Qy        196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1523 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1582

Qy        256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
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Db       1583 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 1642

Qy        316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1643 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 1702

Qy        376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1763 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 1822

Qy        496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555
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Db       1823 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 1882

Qy        556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1883 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 1942

Qy        616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1943 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 2002
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Qy       676 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 735
Db      2003 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 2062

Qy       736 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 795
Db      2063 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 2122

Qy       796 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 855
Db      2123 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 2182

Qy       856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
Db      2183 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 2242

Qy       916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
Db      2243 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 2302

Qy       976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035
Db      2303 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 2362

Qy      1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
Db      2363 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 2422

Qy      1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155
Db      2423 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 2482

Qy      1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215
Db      2483 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 2542

Qy      1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275
Db      2543 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 2602

Qy      1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335
Db      2603 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 2662

Qy      1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395
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Db      2783 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 2842

Qy      1516 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 1575
Db      2843 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 2902

Qy      1576 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 1635
Db      2903 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 2962

Qy      1636 AGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 1695
Db      2963 AGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 3022

Qy      1696 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 1755
Db      3023 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 3082

Qy      1756 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG 1815
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Qy      1816 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 1875
Db      3143 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 3202

Qy      1876 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------- 1915
Db      3203 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTG 3262

Qy      1916 ---------- 1915
Db      3263 GCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTG 3322

Qy      1916 ---------- 1915
Db      3323 CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATT 3382

Qy      1916 ----------CCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 1948
Db      3383 TTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 3442

Qy      1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008
Db      3443 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 3502

Qy      2009 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 2068
Db      3503 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 3562

Qy      2069 GGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 2128
Db      3563 GGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 3622

Qy      2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
Db      3623 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 3674
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RESULT 6
AAH76383
ID   AAH76383 standard; cDNA; 3900 BP.
XX
AC   AAH76383;
XX
DT   30-NOV-2001  (first entry)
XX
DE   Human TLCC polypeptide encoding cDNA.
XX
KW   TLCC; transient receptor potential; TRP; TRP-like calcium channel; human;
KW   hepatotropic; cardiant; antiarteriosclerotic; antiinflammatory; virucide;
KW   cytostatic; analgesic; cerebroprotective; nootropic; neuroprotective;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             138. .3527
FT                   /*tag=  a
FT                   /product= "TLCC polypeptide"
FT                   /note= "coding sequence (AAH76384) specifically claimed"
XX
PN   WO200162794-A2.
XX
PD   30-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US005529.
XX
PR   22-FEB-2000; 2000US-00510706.
PR   31-MAY-2000; 2000US-00583373.
PR   08-AUG-2000; 2000US-00634669.
XX
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PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Glucksmann MA, Curtis RAJ, Lora JM;
XX
DR WPI; 2001-557700/62.
DR P-PSDB; AAB85974.
XX
PT New isolated nucleic acid encoding a transient receptor potential-like
PT calcium channel for identifying modulators that can be used to treat
PT hepatic or cardiovascular disorders.
XX
PS Claim 1; Fig 1A-D; 160pp; English.
XX
CC The invention provides isolated nucleic acids encoding a human transient
CC receptor potential (TRP) family member, called TRP-like calcium channel
CC (TLCC) polypeptide. The TLCC polypeptide can be expressed by standard
CC recombinant methodology. The TLCC polynucleotides and polypeptide are
CC used to identify modulators that can be used to treat a hepatic or a
CC cardiovascular disorder, such as liver fibrosis or atherosclerosis. Other
CC disorders that can be treated are hepatitis, liver tumours, cirrhosis of
CC the liver, hemochromatosis, liver parasite induced disorders, central
CC nervous system disorders, pain disorders, or disorders of cellular
CC growth, differentiation or migration. The TLCC polynucleotides,
CC polypeptide, protein homologs and antibodies to the proteins can be used
CC in predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials and pharmacogenetics). Anti-TLCC antibodies
CC can isolate TLCC proteins, regulate the bioavailablility of TLCC
CC proteins, and modulate TLCC activity. The present sequence represents a
CC cDNA encoding the human TLCC polypeptide
XX
SQ Sequence 3900 BP; 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;

Query Match 90.8%; Score 1978.8; DB 5; Length 3900;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;

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Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
              | | | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1530 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1589

Qy         76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1590 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 1649

Qy        136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 1709

Qy        196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1710 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1769

Qy        256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
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Db       1770 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 1829

Qy        316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
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Db       1830 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 1889

Qy        376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1890 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 1949

Qy        436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
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Db       1950 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 2009

Qy        496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2010 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 2069

Qy        556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
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Db       2070 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 2129

Qy        616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2130 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 2189

Qy        676 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 735
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2190 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 2249

Qy        736 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 795
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2250 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 2309

Qy        796 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 855
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2310 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 2369

Qy        856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
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Db       2370 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 2429

Qy        916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
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Qy        976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2550 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 2609

Qy       1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2610 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 2669

Qy       1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215
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Qy       1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2790 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 2849

Qy       1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2850 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 2909

Qy       1396 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 1455
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Qy       1516 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 1575
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Db       3090 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 3149

Qy       1636 AGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 1695
              ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
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Db       3150 AGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 3209

Qy       1696 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 1755
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3210 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 3269

Qy       1756 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG 1815
             ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
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Qy       1816 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 1875
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             |||||||||||||||||||||||||||||||||||||||
Db       3390 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTG 3449

Qy       1916 ---------- 1915

Db       3450 GCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTG 3509

Qy       1916 ---------- 1915

Db       3510 CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATT 3569

Qy       1916 ----------CCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 1948
                         ||||||||||||||||||||||||||||||||
Db       3570 TTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 3629

Qy       1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3630 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 3689

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Db       3690 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 3749

Qy       2069 GGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 2128
             |||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3750 GGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 3809

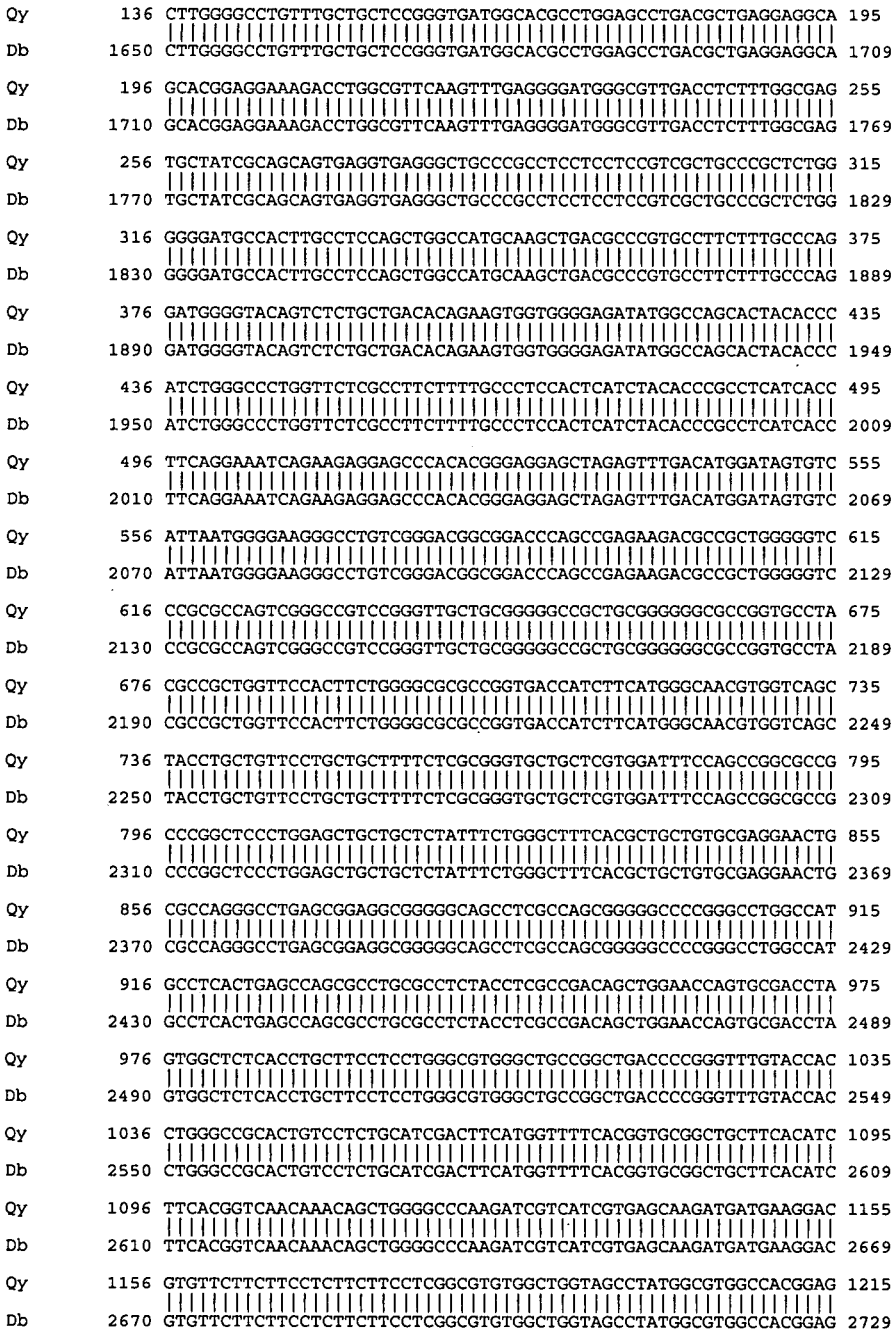
Qy       2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
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Db       3810 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 3861
```

RESULT 7
ABS58041
ID ABS58041 standard; cDNA; 3900 BP.
XX
AC ABS58041;
XX
DT 14-FEB-2003 (first entry)
XX
DE Human transient receptor potential (TRP)-like calcium channel (TLCC).
XX
KW Human; gene; ss; transient receptor potential-like calcium channel; TRP;
KW TLCC; 18607; calcium signalling; growth; differentiation;
KW capacitative calcium channel; store-operated calcium channel; SOC;
KW plasma membrane; calcium ion; cytosol; modulator; membrane excitability;
KW action potential; excitation; neurite outgrowth; synaptogenesis;
KW signal transduction; angiogenesis; cell proliferation; vascular tone;
KW gene therapy; diagnosis; cardiovascular disorder; atherosclerosis;
KW restenosis; endothelial cell disorder; tumour metastasis; psoriasis;
KW rheumatoid arthritis; diabetes; hepatic disorder; hepatitis; cirrhosis;
KW central nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; multiple sclerosis; epilepsy; cancer;
KW cellular proliferation disorder; migration disorder; therapeutic.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT 5'UTR   1. .137
FT   /*tag= a
FT CDS   138. .3390
FT   /*tag= b
FT   /product= "TLCC"
FT   /note= "This CDS is specifically claimed in claim 1"
FT 3'UTR   3391. .3900
FT   /*tag= c
XX
PN US2002142377-A1.
XX
PD 03-OCT-2002.
XX
PF 20-FEB-2001; 2001US-00789481.
XX
PR 22-FEB-2000; 2000US-00510706.
PR 31-MAY-2000; 2000US-00583373.
PR 08-AUG-2000; 2000US-00634669.
XX
PA (GLUC/) GLUCKSMANN M A.
PA (CURT/) CURTIS R A J.
PA (LORA/) LORA J M.
XX
PI Glucksmann MA, Curtis RAJ, Lora JM;
XX
DR WPI; 2003-102516/09.
DR P-PSDB; ABG72088.
XX
PT Isolated transient receptor potential-like calcium channel polypeptide,
PT useful for treating cardiovascular, hepatic, central nervous system
PT disorders, pain, cellular proliferation, or migration disorder.
XX
PS Claim 1; Fig 1; 80pp; English.
XX
CC The invention discloses an isolated transient receptor potential (TRP)-
CC like calcium channel (TLCC) polypeptide (18607). Calcium signalling has
CC been implicated in the regulation of a variety of cellular responses,
CC such as growth and differentiation. TLCC is a member of the capacitative
CC calcium channel group or store-operated calcium channel (SOC) which is
CC activated in the plasma membrane to import calcium ions from the
CC extracellular environment to the cytosol. The nucleic acids, polypeptides
CC and antibodies of TLCC are useful for detecting its presence in a sample,
CC for identifying a compound which binds to it and identifying a compound
CC which modulates its activity. Modulators of TLCC can be used to modulate
CC membrane excitability, wave forms and frequencies of action potentials,
CC thresholds of excitation, neurite outgrowth and synaptogenesis, signal
CC transduction, angiogenesis, endothelial cell proliferation and vascular
CC tone. The nucleic acid and polypeptide are also useful (using gene
CC therapy) for diagnosing and treating cardiovascular disorders, such as
CC atherosclerosis and restenosis, endothelial cell disorders, such as
CC tumour metastasis, psoriasis, rheumatoid arthritis and diabetes, hepatic
CC disorders such hepatitis and cirrhosis, central nervous system disorders,
CC such as Alzheimer's disease, Parkinson's disease, multiple sclerosis and
CC epilepsy, cellular proliferation disorders, such as cancer, and growth,
CC differentiation or migration disorders. TLCC can also be used in
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials and pharmacogenomics) and in methods of
CC treatment (e.g. therapeutic and prophylactic). The sequence presented is
CC the human TLCC, 18607, cDNA
XX
SQ Sequence 3900 BP; 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;

  Query Match   90.8%; Score 1978.8; DB 8; Length 3900;
  Best Local Similarity   92.5%; Pred. No. 0;
  Matches 2157; Conservative   3; Mismatches   5; Indels 167; Gaps   1;

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Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
              | | | | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1530 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1589

Qy         76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1590 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 1649
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Qy 136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
Db 1650 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 1709
Qy 196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
Db 1710 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1769
Qy 256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
Db 1770 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 1829
Qy 316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
Db 1830 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 1889
Qy 376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
Db 1890 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 1949
Qy 436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
Db 1950 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 2009
Qy 496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555
Db 2010 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 2069
Qy 556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
Db 2070 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 2129
Qy 616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
Db 2130 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 2189
Qy 676 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 735
Db 2190 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 2249
Qy 736 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 795
Db 2250 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 2309
Qy 796 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 855
Db 2310 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 2369
Qy 856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
Db 2370 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 2429
Qy 916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
Db 2430 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 2489
Qy 976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035
Db 2490 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 2549
Qy 1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
Db 2550 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 2609
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Qy 1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215
Db 2670 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 2729
Qy 1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275
Db 2730 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 2789
Qy 1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335
Db 2790 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 2849
Qy 1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395
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Qy 1396 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 1455
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Qy 1636 AGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 1695
Db 3150 AGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 3209
Qy 1696 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 1755
Db 3210 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 3269
Qy 1756 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG 1815
Db 3270 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAG 3329
Qy 1816 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 1875
Db 3330 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 3389
Qy 1876 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------- 1915
Db 3390 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTG 3449
Qy 1916 ---------- 1915
Db 3450 GCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTG 3509
Qy 1916 ---------- 1915
Db 3510 CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATT 3569
Qy 1916 ----------CCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 1948
Db 3570 TTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 3629
Qy 1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008
Db 3630 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 3689
Qy 2009 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 2068
Db 3690 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 3749
Qy 2069 GGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 2128
Db 3750 GGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 3809
Qy 2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180

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                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3810 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 3861


RESULT 8
ADH51622
ID   ADH51622 standard; cDNA; 3900 BP.
XX
AC   ADH51622;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human 18607 protein cDNA sequence.
XX
KW   cytostatic; vasotropic; haemostatic; nephrotropic; gastrointestinal-Gen;
KW   respiratory-Gen; muscular-Gen; osteopathic; antiinflammatory;
KW   immunosuppressive; cardiovascular-Gen; hepatotropic; virucide; analgesic;
KW   antianaemic; endocrine-Gen; neuroprotective; nootropic; cardiant;
KW   gene therapy; cellular proliferative; differentiative disorder; brain;
KW   blood vessel; platelet; breast; colon; kidney; lung; ovarian; prostate;
KW   pancreatic; skeletal muscle; testicular; hormonal; bone metabolism;
KW   immune disorder; inflammatory disorder; cardiovascular disorder;
KW   endothelial cell; liver; viral; pain; metabolic; anaemia; angiogenesic;
KW   neoplastic; endocrine disorder; neurological; heart; tissue typing;
KW   chromosomal mapping; predictive medicine; pharmacogenomic; human; gene;
KW   ss; 18607.
XX
OS   Homo sapiens.
XX
PN   US2003219806-A1.
XX
PD   27-NOV-2003.
XX
PF   18-MAR-2003; 2003US-00391399.
XX
PR   22-FEB-2000; 2000US-00510706.
PR   07-APR-2000; 2000US-0195734P.
PR   31-MAY-2000; 2000US-00583373.
PR   26-JUN-2000; 2000US-0214176P.
PR   08-AUG-2000; 2000US-00634669.
PR   31-AUG-2000; 2000US-0229036P.
PR   19-SEP-2000; 2000US-0233537P.
PR   01-FEB-2001; 2001US-0267076P.
PR   20-FEB-2001; 2001US-00789481.
PR   12-MAR-2001; 2001US-0275078P.
PR   12-MAR-2001; 2001US-0275172P.
PR   06-APR-2001; 2001US-00828035.
PR   26-JUN-2001; 2001US-00891762.
PR   29-AUG-2001; 2001US-00942447.
PR   17-SEP-2001; 2001US-0322983P.
PR   19-SEP-2001; 2001US-00957683.
PR   27-SEP-2001; 2001US-0325854P.
PR   04-DEC-2001; 2001US-0336936P.
PR   31-JAN-2002; 2002US-00062937.
PR   08-MAR-2002; 2002US-00094214.
PR   11-MAR-2002; 2002US-00095139.
PR   17-SEP-2002; 2002US-00245121.
PR   26-SEP-2002; 2002US-00255532.
PR   04-DEC-2002; 2002US-00309804.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Glucksmann MA,  Curtis RAJ,  Lora JM,  Galvin KM,  Silos-Santiago I;
XX
DR   WPI; 2004-010868/01.
DR   P-PSDB; ADH51623.
XX
PT   New 18607, 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324,
PT   55063, 52991, 59914, 59921 or 33751 nucleic acid molecule or polypeptide,
PT   useful for diagnosing, preventing or treating e.g. proliferative or brain
PT   disorders.
XX
PS   Claim 1; SEQ ID NO 1; 276pp; English.
XX
CC   This invention relates to novel human DNA sequences (designated 18607,
CC   15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324, 55063,
CC   52991, 59914, 59921 or 33751) and the proteins encoded by them. The
CC   invention may be useful for the development of compounds with a
CC   cytostatic, vasotropic, haemostatic, nephrotropic, gastrointestinal-Gen,
CC   respiratory-Gen, muscular-Gen, osteopathic, antiinflammatory,
CC   immunosuppressive, cardiovascular-Gen, hepatotropic, virucide, analgesic,
CC   antianaemic, endocrine-Gen, neuroprotective, nootropic or cardiant
CC   activity. In addition, the sequences may be useful for gene therapy. The
CC   invention may be useful in diagnosing, preventing or treating disorders
CC   characterised by aberrant 18607, 15603, 69318, 12303, 48000, 52920, 5433,
CC   38554, 57301, 58324, 55063, 52991, 59914, 59921 or 33751 activity, for
CC   example cellular proliferative and/or differentiative disorder, brain
CC   disorder, blood vessel disorder, platelet disorder, breast disorder,
CC   colon disorder, kidney disorder, lung disorder, ovarian disorder,
CC   prostate disorder, pancreatic disorder, skeletal muscle disorder,
CC   testicular disorder, hormonal disorder, disorder associated with bone
CC   metabolism, immune disorder, inflammatory disorder, cardiovascular
CC   disorder, endothelial cell disorder, liver disorder, viral disease, pain,
CC   metabolic disorder, anaemia, angiogenesic disorder, neoplastic disorder,
CC   endocrine disorder, neurological disorder or heart disorder. They may
CC   also be used in screening assays, tissue typing, chromosomal mapping,
CC   predictive medicine or pharmacogenomics. The present sequence is that of
CC   the cDNA which encodes the human 18607 protein of the invention.
XX
SQ   Sequence 3900 BP; 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;

  Query Match           90.8%;  Score 1978.8;  DB 12;  Length 3900;
  Best Local Similarity   92.5%;  Pred. No. 0;
  Matches 2157;  Conservative    3;  Mismatches    5;  Indels  167;  Gaps    1;

Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
              | | | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1530 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1589

Qy         76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1590 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 1649

Qy        136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 1709

Qy        196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1710 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1769

Qy        256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1770 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 1829

Qy        316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1830 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 1889

Qy        376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1890 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 1949

Qy        436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1950 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 2009

Qy        496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2010 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 2069

Qy        556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
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Db       2070 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 2129

Qy        616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
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Db       2130 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 2189

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Db       2190 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 2249

Qy        736 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 795

Db       2250 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 2309

Qy        796 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 855

Db       2310 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 2369

Qy        856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915

Db       2370 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 2429

Qy        916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975

Db       2430 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 2489

Qy        976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035

Db       2490 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 2549

Qy       1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095

Db       2550 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 2609

Qy       1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155

Db       2610 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 2669

Qy       1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215

Db       2670 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 2729

Qy       1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275

Db       2730 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 2789

Qy       1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335

Db       2790 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 2849

Qy       1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395

Db       2850 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 2909

Qy       1396 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 1455

Db       2910 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 2969

Qy       1456 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 1515

Db       2970 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 3029

Qy       1516 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 1575

Db       3030 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 3089

Qy       1576 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 1635

Db       3090 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 3149

Qy       1636 AGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 1695

Db       3150 AGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 3209

Qy       1696 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 1755

Db       3210 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 3269

Qy       1756 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG 1815

Db       3270 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAG 3329

Qy       1816 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 1875

Db       3330 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 3389

Qy       1876 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------- 1915

Db       3390 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTG 3449

Qy       1916 ---------- 1915

Db       3450 GCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTG 3509

Qy       1916 ---------- 1915

Db       3510 CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATT 3569

Qy       1916 ----------CCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 1948

Db       3570 TTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 3629

Qy       1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008

Db       3630 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 3689

Qy       2009 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 2068

Db       3690 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 3749

Qy       2069 GGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 2128

Db       3750 GGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 3809

Qy       2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180

Db       3810 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 3861
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RESULT 9
AAA49923
ID   AAA49923 standard; cDNA; 4061 BP.
XX
AC   AAA49923;
XX
DT   10-OCT-2000  (first entry)
XX
DE   Human calcium channel SOC-3/CRAC-2 cDNA.
XX
KW   SOC-2/CRAC-1; calcium channel; human; store operated channel;
KW   calcium release activated channel; therapy; diagnosis;
KW   lymphocyte proliferative disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             382. .5979
FT                   /*tag=  a
XX
PN   WO200040614-A2.
XX
PD   13-JUL-2000.
XX
PF   20-DEC-1999;   99WO-US029996.
XX
PR   30-DEC-1998;   98US-0114220P.
PR   29-JAN-1999;   99US-0120018P.
PR   22-JUN-1999;   99US-0140415P.
XX
```

PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Scharenberg AM;
XX
DR WPI; 2000-465957/40.
DR P-PSDB; AAY95436.
XX
PT New SOC/CRAC calcium channel polynucleotides and polypeptides used to
PT diagnose and treat proliferative disorders associated with the channel,
PT and to screen for novel modulators of the channel.
XX
PS Claim 1(a); Page 99-100; 108pp; English.
XX
CC The present sequence is a full-length nucleotide sequence of human SOC-
CC 3/CRAC-2 cDNA. It includes an open reading frame encoding SOC-3/CRAC-2
CC (see AAY95436), a member of a novel family of store operated channel
CC (SOC) or calcium release activated channel (CRAC) polypeptides that
CC modulate Ca2+ flux into and out of a cell, and which may be activated
CC upon depletion of Ca2+ from intracellular calcium stores, allowing Ca2+
CC influx into a cell. SOC-3/CRAC-2 is expressed predominantly in kidney and
CC colon. Compositions for expressing SOC/CRAC calcium channel polypeptides
CC in cells may be useful for treating patients that have reduced
CC extracellular calcium influx into their SOC/CRAC-expressing cells. They
CC will also be useful for delivering therapeutic and/or imaging agents to
CC such cells to modulate proliferation and growth. SOC/CRAC polypeptides
CC also represent targets for designing and/or identifying inhibitors that
CC block lymphocyte proliferation and binding agents that selectively bind
CC to SOC/CRAC polypeptides to which drugs or toxins can be conjugated for
CC delivery to SOC/CRAC expressing cells. SOC/CRAC polynucleotides are used
CC as probes and primers to identify other members of the SOC/CRAC family of
CC calcium channels, as diagnostic reagents for identifying the presence of
CC SOC/CRAC polypeptides in biological samples, as agents for generating
CC SOC/CRAC binding polypeptides, and in gene therapy. Methods for
CC determining the level of SOC/CRAC expression in a subject can be used to
CC assess the presence, or absence, or stage of a proliferative disorder,
CC e.g. a lymphocyte proliferative disorder
XX
SQ Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

Query Match 90.8%; Score 1978.8; DB 3; Length 4061;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;

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Qy        16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
             | | | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1720 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1779

Qy        76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1780 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 1839

Qy       136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1840 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 1899

Qy       196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1900 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1959

Qy       256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1960 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 2019

Qy       316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2020 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 2079

Qy       376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2080 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 2139

Qy       436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2140 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 2199

Qy       496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2200 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 2259

Qy       556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2260 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 2319

Qy       616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2320 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 2379

Qy       676 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2380 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 2439

Qy       736 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 795
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2440 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 2499

Qy       796 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 855
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2500 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 2559

Qy       856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2560 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 2619

Qy       916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2620 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 2679

Qy       976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2680 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 2739

Qy      1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2740 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 2799

Qy      1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2800 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 2859

Qy      1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2860 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 2919

Qy      1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2920 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 2979

Qy      1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2980 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 3039

Qy      1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3040 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 3099

Qy      1396 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 1455
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3100 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 3159

Qy      1456 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 1515
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3160 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 3219

Qy      1516 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 1575
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3220 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 3279
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Qy       1576 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 1635
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3280 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 3339

Qy       1636 AGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 1695
             ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db       3340 AGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 3399

Qy       1696 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 1755
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3400 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 3459

Qy       1756 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG 1815
             ||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db       3460 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAG 3519

Qy       1816 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 1875
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3520 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 3579

Qy       1876 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------------- 1915
             ||||||||||||||||||||||||||||||||||||||
Db       3580 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTG 3639

Qy       1916 ------------------------------------------------------------ 1915

Db       3640 GCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTG 3699

Qy       1916 ------------------------------------------------------------ 1915

Db       3700 CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATT 3759

Qy       1916 ----------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 1948
                                          ||||||||||||||||||||||||||||||||
Db       3760 TTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 3819

Qy       1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008
             ||||||||||||||||||||||||||||||||||||||||||||||||||.||||||||||||
Db       3820 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 3879

Qy       2009 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 2068
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3880 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 3939

Qy       2069 GGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 2128
             |||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3940 GGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 3999

Qy       2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4000 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 4051


RESULT 10
ADH62711
ID   ADH62711 standard; cDNA; 4061 BP.
XX
AC   ADH62711;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Ca activated nonselective transmembrane channel protein TRPM4b cDNA.
XX
KW   bioactive agent; monovalent cation permeability; TRPM4b channel; human;
KW   calcium activated nonselective transmembrane channel; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             73. .3717
FT                   /*tag=  a
FT                   /product= "TRPM4b"
FT                   /note= "Calcium activated nonselective (CAN)
FT                   transmembrane channel protein"
XX
PN   US2003143557-A1.
XX
PD   31-JUL-2003.
XX
PF   08-MAY-2002; 2002US-00142649.
XX
PR   25-JAN-2002; 2002US-0351938P.
PR   02-MAY-2002; 2002US-0377937P.
XX
PA   (PENN/) PENNER R.
XX
PI   Penner R;
XX
DR   WPI; 2003-829785/77.
DR   P-PSDB; ADH62712.
XX
PT   Screening for candidate bioactive agents involves contacting calcium-
PT   activated nonselective transmembrane channel polypeptide designated as
PT   TRPM4b with candidate agent, determining binding of candidate agent
PT   TRPM4b.
XX
PS   Claim 5; SEQ ID NO 1; 25pp; English.
XX
CC   The invention describes a method of screening (M1) for a candidate
CC   bioactive agent (CA) modulating monovalent cation (MC) permeability of
CC   the TRPM4b (I) channel. The method involves providing a recombinant cell
CC   (RC) with a nucleic acid encoding (I) and an inducible promoter operably
CC   linked to (I), capable of expressing (I), and comprises an MC indicator,
CC   inducing RC to express (I), contacting RC with MC and CA, and detecting
CC   intracellular levels of MC with an indicator. The method is useful for
CC   creening for a candidate bioactive agent capable of modulating monovalent
CC   cation permeability of a TRPM4b channel. This sequence encodes human
CC   calcium activated nonselective (CAN) transmembrane channel protein
CC   TRPM4b.
XX
SQ   Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

  Query Match             90.8%;  Score 1978.8;  DB 10;  Length 4061;
  Best Local Similarity   92.5%;  Pred. No. 0;
  Matches 2157;  Conservative    3;  Mismatches    5;  Indels  167;  Gaps    1;

Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
              | | | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1720 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1779

Qy         76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1780 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 1839

Qy        136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1840 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 1899

Qy        196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1900 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1959

Qy        256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1960 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 2019

Qy        316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2020 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 2079

Qy        376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2080 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 2139

Qy        436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
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Db       2140 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 2199

Qy        496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555

Db       2200 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 2259

Qy        556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615

Db       2260 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 2319

Qy        616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675

Db       2320 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 2379

Qy        676 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 735

Db       2380 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 2439

Qy        736 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 795

Db       2440 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 2499

Qy        796 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 855

Db       2500 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 2559

Qy        856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915

Db       2560 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 2619

Qy        916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975

Db       2620 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 2679

Qy        976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035

Db       2680 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 2739

Qy       1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095

Db       2740 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 2799

Qy       1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155

Db       2800 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 2859

Qy       1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215

Db       2860 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 2919

Qy       1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275

Db       2920 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 2979

Qy       1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335

Db       2980 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 3039

Qy       1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395

Db       3040 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 3099

Qy       1396 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 1455

Db       3100 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 3159

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Db       3280 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 3339

Qy       1636 AGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 1695

Db       3340 AGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 3399

Qy       1696 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 1755

Db       3400 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 3459

Qy       1756 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG 1815

Db       3460 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAG 3519

Qy       1816 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 1875

Db       3520 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 3579

Qy       1876 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------- 1915

Db       3580 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTG 3639

Qy       1916 ---------- 1915

Db       3640 GCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTG 3699

Qy       1916 ---------- 1915

Db       3700 CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATT 3759

Qy       1916 ----------CCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 1948

Db       3760 TTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 3819

Qy       1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008

Db       3820 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 3879

Qy       2009 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 2068

Db       3880 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 3939

Qy       2069 GGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 2128

Db       3940 GGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 3999

Qy       2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180

Db       4000 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 4051
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RESULT 11
ADR73511
ID   ADR73511 standard; DNA; 4061 BP.
XX
AC   ADR73511;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human TRPM4, gene.
XX
KW   TRPM4; apoptosis; inhibitor; tumour; cytostatic; cancer; gene; ds.
XX
OS   Homo sapiens.
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FH   Key             Location/Qualifiers
FT   CDS             73. .3717
FT                   /*tag=  a
FT                   /product= "Human TRPM4"
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PN WO2004076682-A2.
XX
PD 10-SEP-2004.
XX
PF 26-FEB-2004; 2004WO-US006020.
XX
PR 26-FEB-2003; 2003US-0450886P.
XX
PA (SURR-) SURROMED INC.
XX
PI Axenovich SA, Stull R, Gelman M, Chui K, Ng D;
XX
DR WPI; 2004-653428/63.
DR P-PSDB; ADR73512.
XX
PT Identifying a compound for inducing apoptosis, useful for diagnosing and
PT treating cancer, comprises identifying an inhibitor of a target.
XX
PS Example 1; SEQ ID NO 79; 255pp; English.
XX
CC The invention relates to a novel method for identifying a compound for
CC inducing apoptosis comprises identifying an inhibitor of a target.
CC Examples of an inhibitor of a target include: angio-associated, migratory
CC cell protein (AAMP), disintegrin and metalloproteinase domain 8 (ADAM8),
CC disintegrin-like and metalloprotease (reporlysin type) with
CC thrombospondin type 1 motif, 17 (ADAMTS17), adenylate cyclase 3 (ADCY3),
CC adrenergic beta receptor kinase 1 (ADRBK1), bladder cancer associated
CC protein (BLCAP), chromosome 22 open reading frame 5 (C22orf5), CD81
CC antigen (target of antiproliferative antibody 1 (CD81), CD9 antigen (p24)
CC (CD9), claudin 4 (CLDN4), chloride intracellular channel 1 (CLIC1),
CC collagen, type VI, alpha 2 (COL6A2), CTL2, endothelin converting enzyme 1
CC (ECE1), ephrinB1 (EFNB1), flotillin 2 (FLOT2), intercellular adhesion
CC molecule 3 (ICAM3), iduronate 2-sulfatase (Hunter syndrome) (IDS), jagged
CC 2 (JAG2), junctional adhesion molecule 1 (JAM1), lectin, galactoside-
CC binding soluble 3 binding protein (LGALS3BP), similar to possible G-
CC protein receptor (LOC146330), CGI-78 protein (LOC51107), lipoprotein
CC lipase (LPL), low density lipoprotein receptor-related protein 5 (LRP5),
CC Lutheran blood group (Auberger b antigen included) (LU), membrane
CC component, chromosome11, surface marker 1 (M11S1), serum constituent
CC protein (MSE55), neuropathy target esterase (NTE), Homo sapiens cDNA
CC FL31043 fis, clone HSYRA2000248 (PLEXIN A1) or Homo sapiens cDNA FLJ44113
CC fis, clone TESTI4046487, highly similar to Mus musculus plexin A1
CC (PLXNA1), protein tyrosine phosphatase, receptor type, f polypeptide
CC (PTPRF), interacting protein) (liprin), alpha 3 (PPFIA3), Homo sapiens
CC peptide-histidine transporter 4 (PTR4), mRNA (PTR4), solute carrier
CC family 16 (monocarboxylic acid transporters) member 3 (SLC16A3), solute
CC carrier family 1 (neutral amino acid transporter) member 5 (SLC1A5),
CC solute carrier family 39 (zinc transporter) member 3 (SLC39A1), serine
CC protease inhibitor, Kunitz type 2 (SPINT2), stanniocalcin 2 (STC2),
CC tumour necrosis receptor superfamily member 21 (TNFRSF21), tumour
CC rejection antigen (gp96) 1 (TRA1), or transient receptor potential cation
CC channel, subfamily M member 4 (TRPM4), respectively comprising any of the
CC 40 sequences of 87-1615 amino acids (the even numbers selected from SEQ
CC ID:2-80), shown in the specification. The invention further comprises a
CC method for inducing apoptosis and a method for diagnosing a tumour. The
CC novel compounds have cytostatic activity. The method is useful for
CC identifying a compound for inducing apoptosis. The methods and compounds
CC are useful for diagnosing and treating cancer, and in determining the
CC prognosis for cancer in the patient or the susceptibility of the patient
CC to a therapeutic treatment. This polynucleotide sequence represents a
CC gene encoding one of the 40 protein targets of the invention.
XX
SQ Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

Query Match 90.8%; Score 1978.8; DB 13; Length 4061;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;

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Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
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Db       1720 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1779

Qy         76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1780 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 1839

Qy        136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
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Qy        196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
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Qy        256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
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Qy        316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
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Db       2020 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 2079

Qy        376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
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Db       2080 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 2139

Qy        436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
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Db       2140 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 2199

Qy        496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555
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Qy        556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
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Db       2260 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 2319

Qy        616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
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Qy        676 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 735
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Qy        736 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 795
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Db       2440 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 2499

Qy        796 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 855
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Qy        856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
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Qy        916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
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Qy        976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035
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Db       2680 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 2739

Qy       1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
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Qy       1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155
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Qy       1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215
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Db       2860 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 2919

Qy       1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275
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Db       2920 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 2979

Qy       1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335
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Db       2980 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 3039

Qy       1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395
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Qy       1396 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 1455
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Qy       1696 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 1755
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Db       3400 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 3459

Qy       1756 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG 1815
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Qy       1916 ------------------------------------------------------------ 1915

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Qy       1916 ------------------------------------------------------------ 1915

Db       3700 CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATT 3759

Qy       1916 ---------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 1948
                                         |||||||||||||||||||||||||||||||||
Db       3760 TTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 3819

Qy       1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008
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Db       3820 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 3879

Qy       2009 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 2068
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Db       3880 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 3939

Qy       2069 GGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 2128
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Qy       2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
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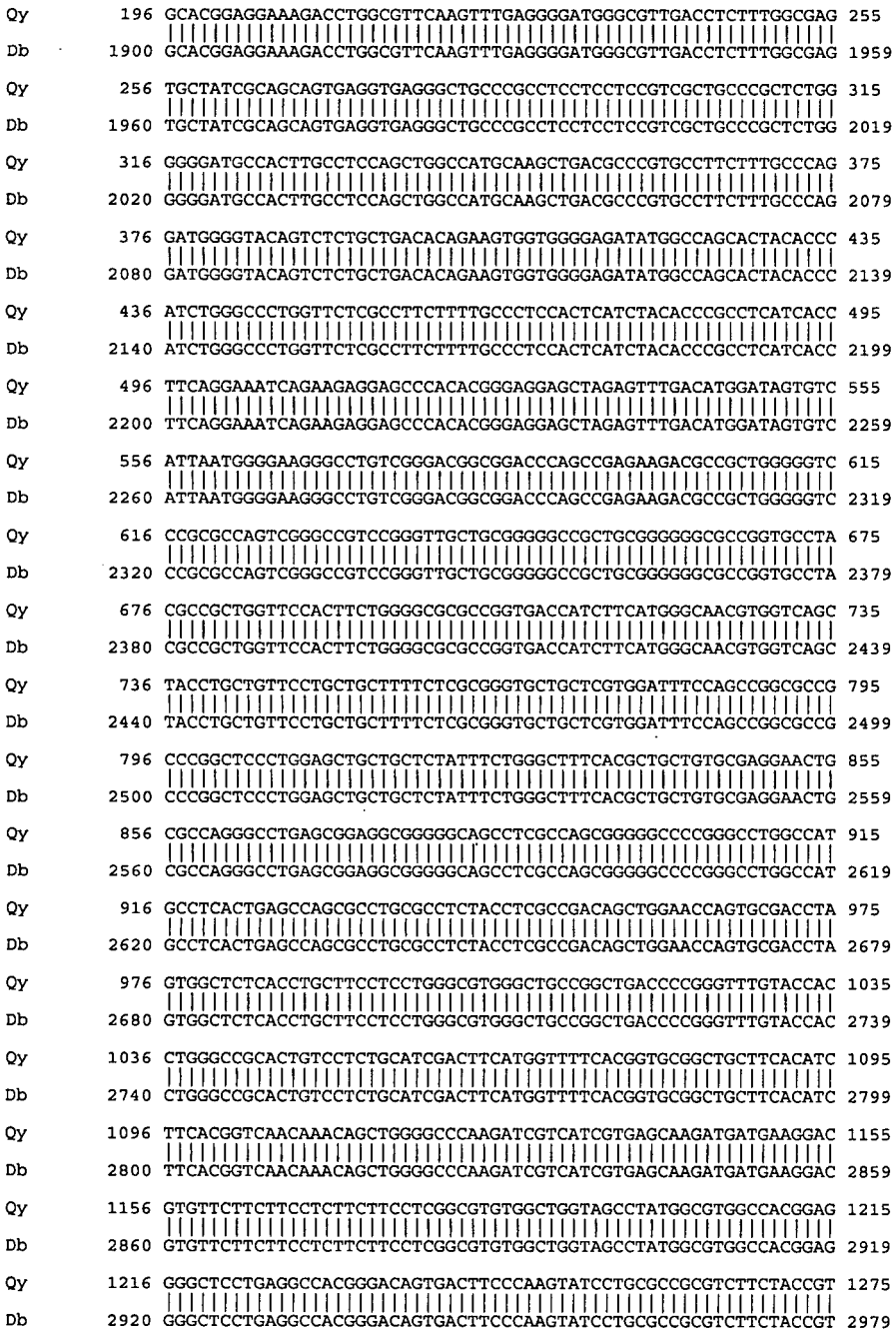
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RESULT 12
ADS12774
ID   ADS12774 standard; cDNA; 4061 BP.
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AC   ADS12774;
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DT   16-DEC-2004  (first entry)
XX
DE   Transient receptor potential cation channel, subfamily M member 4b cDNA.
XX
KW   transient receptor potential cation channel; subfamily M; member 4;
KW   TRPM4; phospholipase A1-A; PLA1A; butyryl coenzyme A synthetase 1; BUCS1;
KW   prostate cancer; TRPM4b; gene; ss.
XX
OS   Homo sapiens.
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FH   Key             Location/Qualifiers
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FT                   /product= "Human TRPM4b protein"
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PN   JP2004267118-A.
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PF   10-MAR-2003; 2003JP-00063578.
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PR   10-MAR-2003; 2003JP-00063578.
XX
PA   (SANY ) SANKYO CO LTD.
XX
DR   WPI; 2004-693915/68.
DR   P-PSDB; ADS12775.
XX
PT   Detecting prostatic cancer, comprises extracting RNA fractions from test
PT   substance of subject and normal human, measuring and analyzing the
PT   difference in e.g., phospholipase A1-A and butyryl coenzyme A synthetase
PT   expression levels.
XX
PS   Claim 1; SEQ ID NO 1; 126pp; Japanese.
XX
CC   The invention comprises a method for detecting prostatic cancer in a
CC   subject. The method involves measuring the expression levels of specific
CC   genes: transient receptor potential cation channel, subfamily M, member 4
CC   (TRPM4); phospholipase A1-A (PLA1A); and butyryl coenzyme A synthetase 1
CC   (BUCS1). The method of the invention is useful for the detection and
CC   treatment of prostate cancer. The present cDNA sequence encodes the human
CC   TRPM4b protein of the invention.
XX
SQ   Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

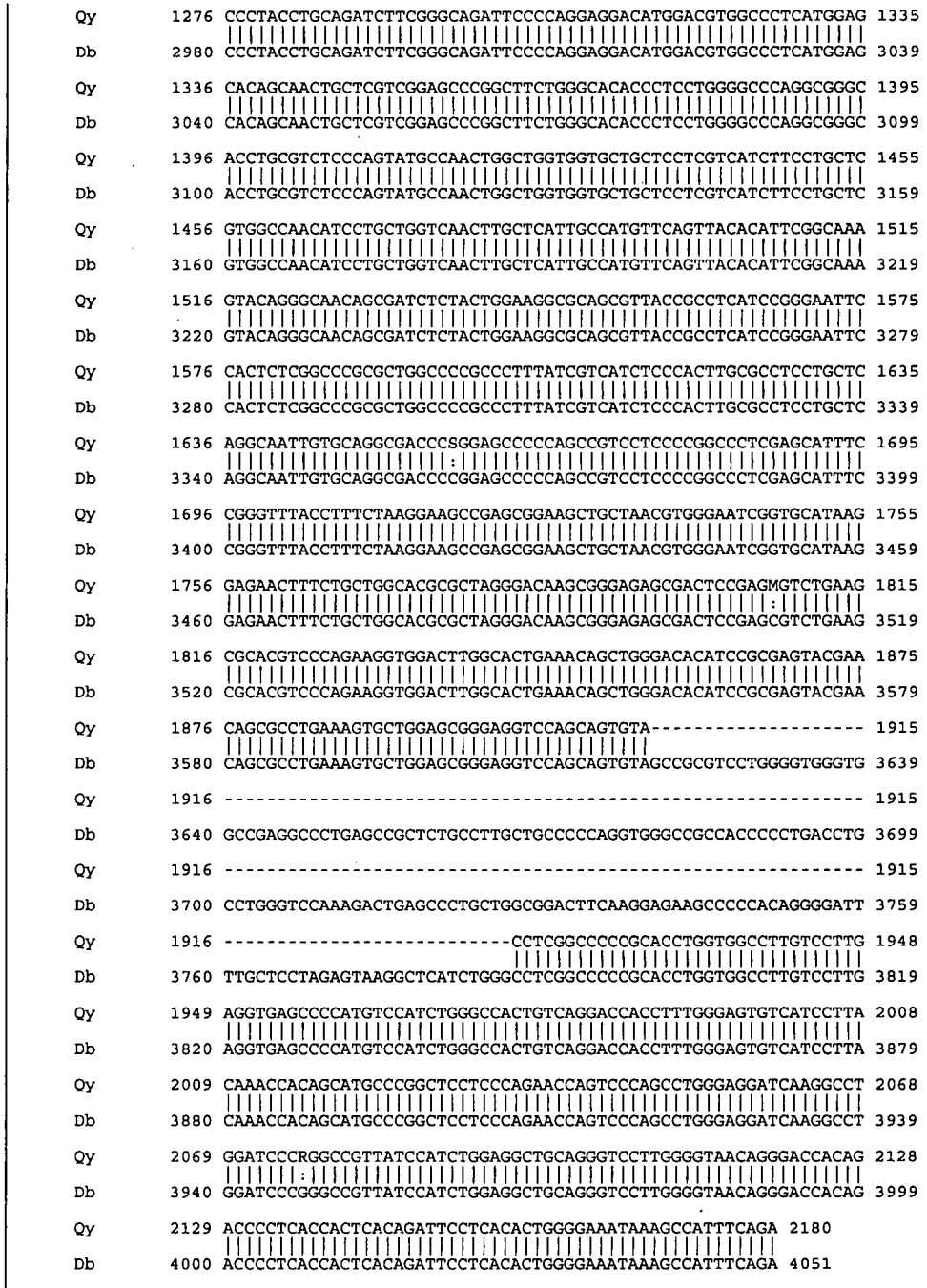
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Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
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Db       1720 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1779

Qy         76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1780 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 1839

Qy        136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
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Db       1840 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 1899
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Qy 196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
Db 1900 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1959
Qy 256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
Db 1960 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 2019
Qy 316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
Db 2020 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 2079
Qy 376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
Db 2080 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 2139
Qy 436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
Db 2140 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 2199
Qy 496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555
Db 2200 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 2259
Qy 556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
Db 2260 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 2319
Qy 616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
Db 2320 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 2379
Qy 676 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 735
Db 2380 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 2439
Qy 736 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 795
Db 2440 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 2499
Qy 796 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 855
Db 2500 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 2559
Qy 856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
Db 2560 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 2619
Qy 916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
Db 2620 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 2679
Qy 976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035
Db 2680 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 2739
Qy 1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
Db 2740 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 2799
Qy 1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155
Db 2800 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 2859
Qy 1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215
Db 2860 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 2919
Qy 1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275
Db 2920 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 2979


Qy 1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335
Db 2980 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 3039
Qy 1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395
Db 3040 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 3099
Qy 1396 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 1455
Db 3100 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 3159
Qy 1456 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 1515
Db 3160 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 3219
Qy 1516 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 1575
Db 3220 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 3279
Qy 1576 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 1635
Db 3280 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 3339
Qy 1636 AGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 1695
Db 3340 AGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 3399
Qy 1696 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 1755
Db 3400 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 3459
Qy 1756 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG 1815
Db 3460 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAG 3519
Qy 1816 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 1875
Db 3520 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 3579
Qy 1876 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------- 1915
Db 3580 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTG 3639
Qy 1916 ---------- 1915
Db 3640 GCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTG 3699
Qy 1916 ---------- 1915
Db 3700 CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATT 3759
Qy 1916 ----------CCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 1948
Db 3760 TTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 3819
Qy 1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008
Db 3820 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 3879
Qy 2009 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 2068
Db 3880 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 3939
Qy 2069 GGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 2128
Db 3940 GGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 3999
Qy 2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
Db 4000 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 4051

RESULT 13
ADN39239
ID ADN39239 standard; cDNA; 4641 BP.
XX
AC ADN39239;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:557.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnerary; gene therapy; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003042661-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR WPI; 2003-468649/44.
DR P-PSDB; ADN39240.
XX
PT Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
PS Claim 8; SEQ ID NO 557; 1385pp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularistaion syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.
XX
SQ Sequence 4641 BP; 808 A; 1459 C; 1432 G; 942 T; 0 U; 0 Other;

Query Match 90.8%; Score 1978.8; DB 11; Length 4641;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;

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Qy        16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
             | | | | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2272 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 2331

Qy        76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2332 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 2391

Qy       136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2392 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 2451

Qy       196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2452 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 2511

Qy       256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2512 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 2571

Qy       316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2572 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 2631

Qy       376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2632 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 2691

Qy       436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2692 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 2751

Qy       496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2752 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 2811

Qy       556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2812 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 2871

Qy       616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2872 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 2931

Qy       676 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2932 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 2991

Qy       736 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 795
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2992 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 3051

Qy       796 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 855
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3052 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 3111

Qy       856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3112 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 3171

Qy       916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3172 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 3231
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Qy       976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3232 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 3291

Qy      1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3292 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 3351

Qy      1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3352 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 3411

Qy      1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3412 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 3471

Qy      1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3472 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 3531

Qy      1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3532 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 3591

Qy      1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3592 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 3651

Qy      1396 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 1455
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3652 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 3711

Qy      1456 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 1515
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3712 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 3771

Qy      1516 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 1575
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3772 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 3831

Qy      1576 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 1635
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Db      3832 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 3891

Qy      1636 AGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 1695
            ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db      3892 AGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 3951

Qy      1696 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 1755
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3952 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 4011

Qy      1756 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG 1815
            ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db      4012 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAG 4071

Qy      1816 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 1875
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4072 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 4131

Qy      1876 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------------- 1915
            ||||||||||||||||||||||||||||||||||||||
Db      4132 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTG 4191

Qy      1916 ------------------------------------------------------------ 1915

Db      4192 GCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTG 4251

Qy      1916 ------------------------------------------------------------ 1915

Db      4252 CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATT 4311
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Qy      1916 ---------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 1948
                                          ||||||||||||||||||||||||||||||||
Db      4312 TTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 4371

Qy      1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4372 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 4431

Qy      2009 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 2068
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4432 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 4491

Qy      2069 GGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 2128
            |||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4492 GGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 4551

Qy      2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4552 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 4603
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RESULT 14
AAD32373
ID AAD32373 standard; cDNA; 2695 BP.
XX
AC AAD32373;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Trp9 splice variant cDNA.
XX
KW Human; prostate carcinoma associated protein; Trp9; Trp10a; Trp10b;
KW transient receptor potential; calcium channel protein; Trp8a; Trp8b;
KW molecular marker; endometrial cancer; uterine carcinoma; melanoma; gene;
KW tumour; chorion carcinoma; lung cancer; antisense therapy;
KW splice variant; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   303. .2339
FT   /*tag= a
FT   /product= "Human Trp9 splice variant protein"
XX
PN WO200210382-A2.
XX
PD 07-FEB-2002.
XX
PF 18-JUL-2001; 2001WO-EP008309.
XX
PR 28-JUL-2000; 2000US-0221513P.
XX
PA (WISS/) WISSENBACH U.
XX
PI Wissenbach U;
XX
DR WPI; 2002-269013/31.
DR P-PSDB; AAE20284.
XX
PT Novel isolated nucleic acid encoding human prostate carcinoma associated
PT protein such as transient receptor potential 8a, 8b, 10a, 10b proteins,
PT useful as molecular markers for diagnosing prostate cancer.
XX
PS Claim 1; Fig 9B; 70pp; English.
XX
CC The invention relates to human prostate carcinoma associated proteins
CC such as transient receptor potential (Trp)8a, Trp8b, Trp9, Trp10a and
CC Trp10b and nucleic acid molecules encoding such polypeptides. Trp8, Trp9,
CC Trp10 are novel calcium channel proteins. Sequences of the invention are
CC useful as molecular markers for diagnosing prostate cancer. Sequences of
CC the invention, their antibodies, inhibitors and antisense molecules are
CC useful for preventing, treating or ameliorating a prostate tumour,
CC endometrial cancer (uterine carcinoma), tumour, a chorion carcinoma,

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CC   cancer of the lung or melanoma. Polynucleotides of the invention are used
CC   in antisense therapy. The present sequence is human Trp9 splice variant
CC   cDNA
XX
SQ   Sequence 2695 BP; 460 A; 873 C; 816 G; 546 T; 0 U; 0 Other;

  Query Match           90.7%;  Score 1977.2;  DB 6;  Length 2695;
  Best Local Similarity  92.5%;  Pred. No. 0;
  Matches 2156;  Conservative    3;  Mismatches    6;  Indels  167;  Gaps    1;

Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
              | | | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 401

Qy         76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 461

Qy        136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 521

Qy        196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 581

Qy        256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        582 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 641

Qy        316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 701

Qy        376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 761

Qy        436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        762 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 821

Qy        496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        822 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 881

Qy        556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        882 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 941

Qy        616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        942 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 1001

Qy        676 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 735
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1002 CGCCGCTGGTTCCACTTCTGGGGCGTGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 1061

Qy        736 TACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCG 795
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Qy        796 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 855
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Qy        856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
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Qy       1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
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Db       1362 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1421

Qy       1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155
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Db       1422 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1481

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Db       2142 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 2201

Qy       1876 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------------- 1915
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Db       2202 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTG 2261

Qy       1916 ------------------------------------------------------------ 1915

Db       2262 GCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTG 2321

Qy       1916 ------------------------------------------------------------ 1915

Db       2322 CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATT 2381
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Qy       1916 ----------------------------CCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 1948
                                          |||||||||||||||||||||||||||||||||
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Qy       1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008
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Db       2442 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2501

Qy       2009 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 2068
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Qy       2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
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RESULT 15
AAD32372
ID AAD32372 standard; cDNA; 4042 BP.
XX
AC AAD32372;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Trp9 protein encoding cDNA.
XX
KW Human; prostate carcinoma associated protein; Trp9; Trp10a; Trp10b;
KW transient receptor potential; calcium channel protein; Trp8a; Trp8b;
KW molecular marker; endometrial cancer; uterine carcinoma; melanoma; gene;
KW tumour; chorion carcinoma; lung cancer; antisense therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 42. .3686
FT /*tag= a
FT /product= "Human Trp9 protein"
XX
PN WO200210382-A2.
XX
PD 07-FEB-2002.
XX
PF 18-JUL-2001; 2001WO-EP008309.
XX
PR 28-JUL-2000; 2000US-0221513P.
XX
PA (WISS/) WISSENBACH U.
XX
PI Wissenbach U;
XX
DR WPI; 2002-269013/31.
DR P-PSDB; AAE20283.
XX
PT Novel isolated nucleic acid encoding human prostate carcinoma associated
PT protein such as transient receptor potential 8a, 8b, 10a, 10b proteins,
PT useful as molecular markers for diagnosing prostate cancer.
XX
PS Claim 1; Fig 9A; 70pp; English.
XX
CC The invention relates to human prostate carcinoma associated proteins
CC such as transient receptor potential (Trp)8a, Trp8b, Trp9, Trp10a and
CC Trp10b and nucleic acid molecules encoding such polypeptides. Trp8, Trp9,
CC Trp10 are novel calcium channel proteins. Sequences of the invention are
CC useful as molecular markers for diagnosing prostate cancer. Sequences of
CC the invention, their antibodies, inhibitors and antisense molecules are
CC useful for preventing, treating or ameliorating a prostate tumour,
CC endometrial cancer (uterine carcinoma), tumour, a chorion carcinoma,
CC cancer of the lung or melanoma. Polynucleotides of the invention are used
CC in antisense therapy. The present sequence is human Trp9 protein encoding
CC cDNA
XX
SQ Sequence 4042 BP; 703 A; 1260 C; 1290 G; 789 T; 0 U; 0 Other;

Query Match 90.7%; Score 1977.2; DB 6; Length 4042;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2156; Conservative 3; Mismatches 6; Indels 167; Gaps 1;

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Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
              | | | |  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1689 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1748

Qy         76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 1868

Qy        196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1869 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1928

Qy        256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
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Qy        316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
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Qy        376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2049 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 2108

Qy        436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
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Qy        496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555
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Qy        556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
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Qy        676 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 735
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Qy      1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
Db      2709 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 2768

Qy      1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155
Db      2769 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 2828

Qy      1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215
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Qy      1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275
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Qy      1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395
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Qy      1636 AGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 1695
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Qy      1696 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 1755
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Db      3429 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAG 3488

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Qy      1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008
Db      3789 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 3848

Qy      2009 CAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCT 2068
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Qy      2069 GGATCCCRGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAG 2128
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Search completed: June 12, 2005, 18:59:17
Job time : 764.137 secs

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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 06:26:36 ; Search time 6141.41 Seconds
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Title: US-09-869-486B-25
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Scoring table: IDENTITY_NUC
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1978.8	90.8	3900	6	AX235183	AX235183 Sequence
3	1978.8	90.8	4042	9	HSA575813	AJ575813 Homo sapi
4	1978.8	90.8	4061	6	BD270156	BD270156 Character
5	1978.8	90.8	4061	9	AF497623	AF497623 Homo sapi
6	1977.2	90.7	2695	6	AX443225	AX443225 Sequence
7	1977.2	90.7	4042	6	AX443227	AX443227 Sequence
8	1975.6	90.6	3810	9	AK000048	AK000048 Homo sapi
9	1974	90.6	3701	9	AY046396	AY046396 Homo sapi
10	1968.2	90.3	3599	6	AX402516	AX402516 Sequence
11	1892.2	86.8	3387	6	AX235185	AX235185 Sequence
12	1892.2	86.8	3402	6	CQ715325	CQ715325 Sequence
13	1892.2	86.8	3523	9	AY297044	AY297044 Homo sapi
14	1892.2	86.8	3879	9	AY297045	AY297045 Homo sapi
15	1891	86.7	2393	6	BD082082	BD082082 Reagents
16	1793.8	82.3	2981	9	AK000235	AK000235 Homo sapi
17	1196	54.9	2737	10	BC046472	BC046472 Mus muscu
18	1196	54.9	2993	10	BC058632	BC058632 Mus muscu
19	1196	54.9	3800	10	MMU575814	AJ575814 Mus muscu
20	1194.4	54.8	3725	10	BC049165	BC049165 Mus muscu
21	1153.2	52.9	1548	6	BD134997	BD134997 Human nuc
22	1153.2	52.9	1548	6	AX018184	AX018184 Sequence
23	1149.8	52.7	1524	6	BD242021	BD242021 Compounds
24	1149.8	52.7	1524	6	AR237204	AR237204 Sequence
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38	1012.2	46.4	3444	9	AY297046	AY297046 Homo sapi
39	896.2	41.1	1297	6	BD082083	BD082083 Reagents
40	876.4	40.2	1906	10	AB040807	AB040807 Rattus no
41	876.2	40.2	2088	10	BC049993	BC049993 Mus muscu
42	828.4	38.0	1467	10	AB112658	AB112658 Mus muscu
43	617	28.3	1378	10	BC046537	BC046537 Mus muscu
44	608.8	27.9	1269	10	AB112657	AB112657 Mus muscu
45	538.6	24.7	3913	6	AX135949	AX135949 Sequence

ALIGNMENTS

RESULT 1
BD270154
LOCUS BD270154 2180 bp DNA linear PAT 17-JUL-2003
DEFINITION Characterization of a calcium channel family.
ACCESSION BD270154
VERSION BD270154.1 GI:33079922
KEYWORDS JP 2002536966-A/13.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2180)
AUTHORS Scharenberg,A.M.
TITLE Characterization of a calcium channel family
JOURNAL Patent: JP 2002536966-A 13 05-NOV-2002;
BETH ISRAEL DEACONESS MEDICAL CENTER INC
COMMENT OS Homo sapiens (human)
PN JP 2002536966-A/13
PD 05-NOV-2002
PF 20-DEC-1999 JP 2000592322
PR 30-DEC-1998 US 60/114220,29-JAN-1999 US 60/120018 PR
22-JUN-1999 US 60/140415
PI ANDREW M SCHARENBERG
PC C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K35/76,A61K38/
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PC A61K39/395,A61K39/395,A61K45/00,A61K48/00,A61P3/14,A61P43/00,
PC C07K14/47,
PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/48,C12Q1/
PC 68,G01N33/15,
PC G01N33/50,G01N33/53,G01N33/566,G01N33/577,C12N15/00,C12N5/00,
PC A61K37/02
CC Characterization of a calcium channel family
FH Key Location/Qualifiers
FT source 1. .2180
FT /organism='Homo sapiens (human)'.
FEATURES Location/Qualifiers
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ORIGIN

Query Match 99.9%; Score 2178.8; DB 6; Length 2180;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 GACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTT 240
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Qy        241 GACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGT 300
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Db       1981 AGGACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAAC 2040

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RESULT 2
AX235183
LOCUS       AX235183               3900 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 1 from Patent WO0162794.
ACCESSION   AX235183
VERSION     AX235183.1  GI:15593774
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Glucksmann,M.A., Curtis,R.A. and Lora,J.M.
  TITLE     18607, a human calcium channel
  JOURNAL   Patent: WO 0162794-A 1 30-AUG-2001;
            Millennium Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           90.8%;  Score 1978.8;  DB 6;  Length 3900;
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Qy        376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
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Qy        556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
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Qy        616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
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Qy        856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
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Qy        916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
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Qy        976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035
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Db       2490 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 2549

Qy       1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
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Db       2550 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 2609

Qy       1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155
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Qy       1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215
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Qy       1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275
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Qy       1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335
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Qy       1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395
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Qy       1916 ------------------------------------------------------------ 1915

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Qy       1916 ------------------------------------------------------------ 1915

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RESULT 3
HSA575813
LOCUS       HSA575813              4042 bp    mRNA    linear   PRI 12-AUG-2003
DEFINITION  Homo sapiens mRNA for transient receptor potential ion channel
            melastatin subgroup member 4 protein (TRPM4 gene).
ACCESSION   AJ575813
VERSION     AJ575813.1  GI:32487283
KEYWORDS    transient receptor potential ion channel melastatin subgroup member
            4 protein; TRPM4 gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nilius,B., Prenen,J., Droogmans,G., Voets,T., Vennekens,R.,
            Freichel,M., Wissenbach,U. and Flockerzi,V.
  TITLE     Voltage Dependence of the Ca2+-activated Cation Channel TRPM4
  JOURNAL   J. Biol. Chem. 278 (33), 30813-30820 (2003)
  MEDLINE   22791733
   PUBMED   12799367
REFERENCE   2  (bases 1 to 4042)
  AUTHORS   Wissenbach,U.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUL-2003) Wissenbach U., University of the Saarland,
            Institue for Pharmacology and Toxicology, 66421 Homburg - Saar,
            Saarland, GERMANY
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                     DLFGECYRSSEVRAARLLLRRCPLWGDATCLQLAMQADARAFFAQDGVQSLLTQKWWG
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ORIGIN

  Query Match             90.8%;  Score 1978.8;  DB 9;  Length 4042;
  Best Local Similarity   92.5%;  Pred. No. 0;
  Matches 2157;  Conservative    3;  Mismatches    5;  Indels  167;  Gaps    1;

Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
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Db       1689 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1748
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Qy        76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
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Qy       136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
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Qy       316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
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Qy       376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
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Qy       436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
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Qy       856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
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Qy       916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
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RESULT 4
BD270156
LOCUS       BD270156                4061 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Characterization of a calcium channel family.
ACCESSION   BD270156
VERSION     BD270156.1  GI:33079924
KEYWORDS    JP 2002536966-A/15.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4061)
  AUTHORS   Scharenberg,A.M.
  TITLE     Characterization of a calcium channel family
  JOURNAL   Patent: JP 2002536966-A 15 05-NOV-2002;
            BETH ISRAEL DEACONESS MEDICAL CENTER INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002536966-A/15
            PD   05-NOV-2002
            PF   20-DEC-1999 JP 2000592322
            PR   30-DEC-1998 US    60/114220,29-JAN-1999 US    60/120018 PR
            22-JUN-1999 US    60/140415
            PI   ANDREW M SCHARENBERG
            PC   C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K35/76,A61K38/
            PC   00,
            PC   A61K39/395,A61K39/395,A61K45/00,A61K48/00,A61P3/14,A61P43/00,
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ORIGIN

  Query Match             90.8%;  Score 1978.8;  DB 6;  Length 4061;
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  Matches 2157;  Conservative    3;  Mismatches    5;  Indels  167;  Gaps    1;

Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
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Qy         76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
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Qy        196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
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ACCESSION   AF497623
VERSION     AF497623.1  GI:20269878
KEYWORDS    .
SOURCE      Homo sapiens (human)
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REFERENCE   1  (bases 1 to 4061)
  AUTHORS   Launay,P., Fleig,A., Perraud,A.L., Scharenberg,A.M., Penner,R. and
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  TITLE     TRPM4 is a Ca2+-activated nonselective cation channel mediating
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  JOURNAL   Cell 109 (3), 397-407 (2002)
  MEDLINE   22011788
   PUBMED   12015988
REFERENCE   2  (bases 1 to 4061)
  AUTHORS   Perraud,A.-L. and Scharenberg,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-APR-2002) Pediatrics, Washington, 1959 NE Pacific
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ORIGIN
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DEFINITION  Sequence 7 from Patent WO0210382.
ACCESSION   AX443225
VERSION     AX443225.1  GI:21690620
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REFERENCE   1
  AUTHORS   Wissenbach,U.
  TITLE     Trp8, trp9 and trp10, markers for cancer
  JOURNAL   Patent: WO 0210382-A 7 07-FEB-2002;
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ORIGIN

  Query Match             90.7%;  Score 1977.2;  DB 6;  Length 2695;
  Best Local Similarity   92.5%;  Pred. No. 0;
  Matches 2156;  Conservative    3;  Mismatches    6;  Indels  167;  Gaps    1;

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DEFINITION Sequence 9 from Patent WO0210382.
ACCESSION AX443227
VERSION AX443227.1 GI:21690622
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Wissenbach,U.
TITLE Trp8, trp9 and trp10, markers for cancer
JOURNAL Patent: WO 0210382-A 9 07-FEB-2002;
Wissenbach, Ulrich (DE)
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ORIGIN

Query Match 90.7%; Score 1977.2; DB 6; Length 4042;
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Qy      1916 ---------- 1915
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Qy      2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
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RESULT 8
AK000048

LOCUS	AK000048 3810 bp mRNA linear PRI 13-SEP-2003
DEFINITION	Homo sapiens cDNA FLJ20041 fis, clone COL00423.
ACCESSION	AK000048
VERSION	AK000048.1 GI:7019878
KEYWORDS	oligo capping; fis (full insert sequence).
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
TITLE	NEDO human cDNA sequencing project
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 3810)
AUTHORS	Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE	Direct Submission
JOURNAL	Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT	NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

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ORIGIN

  Query Match             90.6%;  Score 1975.6;  DB 9;  Length 3810;
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Db       1509 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 1568

Qy        136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
Db       1569 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 1628

Qy        196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
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Qy        256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
Db       1689 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 1748

Qy        316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
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Qy        376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
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Qy        436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
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Qy        556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
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RESULT 9
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LOCUS       AY046396               3701 bp    mRNA    linear   PRI 13-SEP-2001
DEFINITION  Homo sapiens TRP-related cation influx channel (TRPM4) mRNA,
            complete cds.
ACCESSION   AY046396
VERSION     AY046396.1  GI:15617228
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3701)
  AUTHORS   Xu,X.Z., Moebius,F., Gill,D.L. and Montell,C.
  TITLE     Regulation of melastatin, a TRP-related protein, through
            interaction with a cytoplasmic isoform
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (19), 10692-10697 (2001)
  MEDLINE   21438010
   PUBMED   11535825
REFERENCE   2  (bases 1 to 3701)
  AUTHORS   Xu,X.-Z., Moebius,F., Gill,D.L. and Montell,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUL-2001) Biological Chemistry, Johns Hopkins Univ
            School of Medicine, 725 N. Wolfe Street, Baltimore, MD 21205, USA
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ORIGIN
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Qy        436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
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Qy       1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215
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Db       2488 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 2547

Qy       1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275
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Qy       1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335
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Qy       1576 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 1635
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Qy       1876 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA---------------------- 1915
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Qy       1916 ---------------------------------------------------------- 1915

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Qy       1916 ---------------------------------------------------------- 1915

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Qy       1949 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTA 2008
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Qy       2129 ACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 2180
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RESULT 10
AX402516
LOCUS       AX402516               3599 bp    DNA     linear   PAT 07-JUN-2002
DEFINITION  Sequence 88 from Patent WO0198353.
ACCESSION   AX402516
VERSION     AX402516.1  GI:21387507
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hillman,J.L., Tang,Y.T., Yue,H., Elliott,V.S., Tribouley,C.M.,
            Lee,E.A., Ramkumar,J., Lal,P., Xu,Y., Warren,B.A., Hafalia,A.J.,
            Baughn,M.R., Azimzai,Y., Batra,S., Burford,N., Yao,M.G.,
            Nguyen,D.B., Lu,D.A., Walia,N.K., Au-Young,J. and Patterson,C.
  JOURNAL   Patent: WO 0198353-A 88 27-DEC-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

Query Match 90.3%; Score 1968.2; DB 6; Length 3599;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 2147; Conservative 3; Mismatches 6; Indels 167; Gaps 1;

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Qy      16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
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Db    1273 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1332

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Qy     136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
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Db    1393 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 1452

Qy     196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
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Db    1453 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1512

Qy     256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
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Db    1513 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 1572

Qy     316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
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Qy     376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
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Qy     616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
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Qy     856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
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Qy     916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
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Qy     976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035
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Qy    1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
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Qy    1916 ------------------------------------------------------------ 1915

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RESULT 11
AX235185
LOCUS       AX235185               3387 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 3 from Patent WO0162794.
ACCESSION   AX235185
VERSION     AX235185.1  GI:15593776
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Glucksmann,M.A., Curtis,R.A. and Lora,J.M.
  TITLE     18607, a human calcium channel
  JOURNAL   Patent: WO 0162794-A 3 30-AUG-2001;
            Millennium Pharmaceuticals, Inc. (US)
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ORIGIN

  Query Match             86.8%;  Score 1892.2;  DB 6;  Length 3387;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 1897;  Conservative    2;  Mismatches   10;  Indels    0;  Gaps    0;
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Db       1573 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1632

Qy        256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
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Db       1633 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 1692

Qy        316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
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Db       1693 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 1752

Qy        376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
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Qy        436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
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Qy        616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
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Db       1993 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 2052

Qy        676 CGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC 735
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Qy        796 CCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTG 855
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Qy        856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
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Db       2233 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 2292

Qy        916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2293 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 2352

Qy        976 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 1035
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2353 GTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCAC 2412

Qy       1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2413 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 2472

Qy       1096 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 1155
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Db       2473 TTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGAC 2532

Qy       1156 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 1215
Db       2533 GTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAG 2592

Qy       1216 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 1275
Db       2593 GGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGT 2652

Qy       1276 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 1335
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Qy       1336 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 1395
Db       2713 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 2772

Qy       1396 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 1455
Db       2773 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 2832

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Qy       1516 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 1575
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Qy       1576 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 1635
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Qy       1696 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 1755
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Qy       1756 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG 1815
Db       3133 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAG 3192

Qy       1816 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 1875
Db       3193 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 3252

Qy       1876 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTACCTCGGCCC 1924
Db       3253 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCC 3301


RESULT 12
CQ715325
LOCUS       CQ715325               3402 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 1259 from Patent WO02068579.
ACCESSION   CQ715325
VERSION     CQ715325.1  GI:42276182
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 1259 06-SEP-2002;
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            PE Corporation (NY) (US)
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                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
ORIGIN

  Query Match             86.8%;  Score 1892.2;  DB 6;  Length 3402;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 1897;  Conservative    2;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
Db       1405 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1464

Qy         76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
Db       1465 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 1524

Qy        136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
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Qy        196 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 255
Db       1585 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1644

Qy        256 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 315
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Qy        316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
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Qy        376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
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Qy        436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
Db       1825 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 1884

Qy        496 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 555
Db       1885 TTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTC 1944

Qy        556 ATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTC 615
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Qy        616 CCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTA 675
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Db       2245 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 2304

Qy        916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
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Qy      1036 CTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATC 1095
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Qy      1396 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 1455
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Qy      1456 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 1515
Db      2845 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 2904

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Qy      1636 AGGCAATTGTGCAGGCGACCCSGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 1695
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Qy      1876 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTACCTCGGCCC 1924
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RESULT 13
AY297044
LOCUS       AY297044                3523 bp    mRNA    linear   PRI 22-JUL-2003
DEFINITION  Homo sapiens transient receptor potential cation channel subfamily
            M member 4 splice variant A (TRPM4) mRNA, complete cds;
            alternatively spliced.
ACCESSION   AY297044
VERSION     AY297044.1  GI:31335330
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (bases 1 to 3523)
  AUTHORS   Hofmann,T., Chubanov,V., Gudermann,T. and Montell,C.
  TITLE     TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent
            Selective Cation Channel
  JOURNAL   Curr. Biol. 13 (13), 1153-1158 (2003)
  MEDLINE   22726392
   PUBMED   12842017
REFERENCE   2  (bases 1 to 3523)
  AUTHORS   Chubanov,V., Gudermann,T., Hofmann,T. and Montell,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAY-2003) Institut fuer Pharmakologie und
            Toxikologie, Philipps-Universitaet Marburg, Karl-von-Frisch-Strasse
            1, Marburg D-35033, Germany
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ORIGIN

  Query Match           86.8%;  Score 1892.2;  DB 9;  Length 3523;
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Qy        16 CGGCACGAGGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 75
Db      1344 CTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTG 1403

Qy        76 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 135
Db      1404 AACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCT 1463

Qy       136 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 195
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Db      1464 CTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCA 1523

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Db      1524 GCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAG 1583

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Db      1584 TGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGG 1643

Qy       316 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 375
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Db      1644 GGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAG 1703

Qy       376 GATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCC 435
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Qy       436 ATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACC 495
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Qy       856 CGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCAT 915
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Qy       916 GCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTA 975
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RESULT 14
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DEFINITION Homo sapiens transient receptor potential cation channel subfamily M member 4 splice variant B (TRPM4) mRNA, complete cds; alternatively spliced.
ACCESSION AY297045
VERSION AY297045.1 GI:31335332
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3879)
AUTHORS Hofmann,T., Chubanov,V., Gudermann,T. and Montell,C.
TITLE TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent Selective Cation Channel
JOURNAL Curr. Biol. 13 (13), 1153-1158 (2003)
MEDLINE 22726392
PUBMED 12842017
REFERENCE 2 (bases 1 to 3879)
AUTHORS Chubanov,V., Hofmann,T., Gudermann,T. and Montell,C.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-2003) Institut fuer Pharmakologie und Toxikologie, Philipps-Universitaet Marburg, Karl-von-Frisch-Strasse 1, Marburg D-35033, Germany
FEATURES Location/Qualifiers

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ORIGIN

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RESULT 15
BD082082
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DEFINITION  Reagents and methods useful for detecting diseases of the
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ACCESSION   BD082082
VERSION     BD082082.1  GI:22627692
KEYWORDS    JP 2001523948-A/9.
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REFERENCE   1  (bases 1 to 2393)
  AUTHORS   Cohen,M., Friedman,P.N., Gordon,J., Hodges,S.C., Klass,M.R.,
            Kratochvil,J.D., Rapp,L.R., Russell,J.C. and Stroupe,S.D.
  TITLE     Reagents and methods useful for detecting diseases of the prostate
  JOURNAL   Patent: JP 2001523948-A 9 27-NOV-2001;
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COMMENT     PN   JP 2001523948-A/9
            PD   27-NOV-2001
            PF   08-OCT-1997 JP 1998517758
            PR   08-OCT-1996 US    08/727688
            PI   MAURICE COHEN,PAULA N FRIEDMAN,JULIAN GORDON,STEVEN C HODGES,
            PI   MICHAEL R KLASS,JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C  PI
             RUSSELL,
            PI   STEVEN D STROUPE
            PC   C12Q1/68,C07K14/47//C07K16/30,G01N33/574
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ORIGIN

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Qy        707 TGACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGG 766
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Job time : 6167.41 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 06:26:36 ; Search time 11440.5 Seconds
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Title: US-09-869-486B-29
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Scoring table: IDENTITY_NUC
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	3879	95.5	3879	9	AY297045	AY297045 Homo sapi
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10	3384.8	83.3	3523	9	AY297044	AY297044 Homo sapi
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ALIGNMENTS

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LOCUS BD270156 4061 bp DNA linear PAT 17-JUL-2003
DEFINITION Characterization of a calcium channel family.
ACCESSION BD270156
VERSION BD270156.1 GI:33079924
KEYWORDS JP 2002536966-A/15.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4061)
AUTHORS Scharenberg,A.M.
TITLE Characterization of a calcium channel family
JOURNAL Patent: JP 2002536966-A 15 05-NOV-2002;
BETH ISRAEL DEACONESS MEDICAL CENTER INC
COMMENT OS Homo sapiens (human)
PN JP 2002536966-A/15
PD 05-NOV-2002
PF 20-DEC-1999 JP 2000592322
PR 30-DEC-1998 US 60/114220,29-JAN-1999 US 60/120018 PR
22-JUN-1999 US 60/140415
PI ANDREW M SCHARENBERG
PC C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K35/76,A61K38/
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PC A61K39/395,A61K39/395,A61K45/00,A61K48/00,A61P3/14,A61P43/00,
PC C07K14/47,
PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/48,C12Q1/
PC 68,G01N33/15,
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CC Characterization of a calcium channel family
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FT source 1. .4061
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ORIGIN

Query Match 100.0%; Score 4061; DB 6; Length 4061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1621 CCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGC 1680
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Qy    1861 CGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 CGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCG 1920

Qy    1921 TTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1981 AGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAG 2040
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Qy    2101 ACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCC 2160
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Qy       2221 CCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTC 2280
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RESULT 2
AF497623
LOCUS       AF497623                4061 bp    mRNA    linear   PRI 10-MAY-2002
DEFINITION  Homo sapiens cation channel TRPM4B (TRPM4B) mRNA, complete cds.
ACCESSION   AF497623
VERSION     AF497623.1  GI:20269878
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 4061)
  AUTHORS   Launay,P., Fleig,A., Perraud,A.L., Scharenberg,A.M., Penner,R. and
            Kinet,J.P.
  TITLE     TRPM4 is a Ca2+-activated nonselective cation channel mediating
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          cell membrane depolarization
  JOURNAL   Cell 109 (3), 397-407 (2002)
  MEDLINE   22011788
   PUBMED   12015988
REFERENCE   2  (bases 1 to 4061)
  AUTHORS   Perraud,A.-L. and Scharenberg,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-APR-2002) Pediatrics, Washington, 1959 NE Pacific
            Ave, Seattle, WA 98195-6320, USA
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ORIGIN

  Query Match           100.0%;  Score 4061;  DB 9;  Length 4061;
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Qy      2221 CCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTC 2280
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Qy      2341 GGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGG 2400
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HSA575813
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DEFINITION  Homo sapiens mRNA for transient receptor potential ion channel
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ACCESSION   AJ575813
VERSION     AJ575813.1  GI:32487283
KEYWORDS    transient receptor potential ion channel melastatin subgroup member
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nilius,B., Prenen,J., Droogmans,G., Voets,T., Vennekens,R.,
            Freichel,M., Wissenbach,U. and Flockerzi,V.
  TITLE     Voltage Dependence of the Ca2+-activated Cation Channel TRPM4
  JOURNAL   J. Biol. Chem. 278 (33), 30813-30820 (2003)
  MEDLINE   22791733
   PUBMED   12799367
REFERENCE   2  (bases 1 to 4042)
  AUTHORS   Wissenbach,U.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUL-2003) Wissenbach U., University of the Saarland,
            Institue for Pharmacology and Toxicology, 66421 Homburg - Saar,
            Saarland, GERMANY
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RESULT 4
AX443227
LOCUS AX443227 4042 bp DNA linear PAT 02-JUL-2002
DEFINITION Sequence 9 from Patent WO0210382.
ACCESSION AX443227
VERSION AX443227.1 GI:21690622
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Wissenbach,U.
TITLE Trp8, trp9 and trp10, markers for cancer
JOURNAL Patent: WO 0210382-A 9 07-FEB-2002;
Wissenbach, Ulrich (DE)
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ORIGIN

Query Match 99.2%; Score 4028.4; DB 6; Length 4042;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4029; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 5
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ACCESSION   AY297045
VERSION     AY297045.1  GI:31335332
KEYWORDS    .
SOURCE      Homo sapiens (human)
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REFERENCE   1  (bases 1 to 3879)
  AUTHORS   Hofmann,T., Chubanov,V., Gudermann,T. and Montell,C.
  TITLE     TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent
            Selective Cation Channel
  JOURNAL   Curr. Biol. 13 (13), 1153-1158 (2003)
  MEDLINE   22726392
   PUBMED   12842017
REFERENCE   2  (bases 1 to 3879)
  AUTHORS   Chubanov,V., Hofmann,T., Gudermann,T. and Montell,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAY-2003) Institut fuer Pharmakologie und
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            1, Marburg D-35033, Germany
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ORIGIN

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RESULT 6
AK000048
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DEFINITION  Homo sapiens cDNA FLJ20041 fis, clone COL00423.
ACCESSION   AK000048
VERSION     AK000048.1  GI:7019878
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1
  AUTHORS   Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
            Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
            Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3810)
  AUTHORS   Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
            Shibahara,T., Tanaka,T. and Nakamura,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,
            University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1,
            Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp,
            Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            International Trade and Industry of Japan; cDNA full insert
            sequencing: Research Association for Biotechnology; cDNA library
            construction, 5'- & 3'-end one pass sequencing: Departent of
            Virology and Human Genome Center, Institute of Medical Science,
            University of Tokyo (partly supported by Science and Technology
            Agency).
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ORIGIN

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RESULT 7
AX235183
LOCUS       AX235183               3900 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 1 from Patent WO0162794.
ACCESSION   AX235183
VERSION     AX235183.1  GI:15593774
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Glucksmann,M.A., Curtis,R.A. and Lora,J.M.
  TITLE     18607, a human calcium channel
  JOURNAL   Patent: WO 0162794-A 1 30-AUG-2001;
            Millennium Pharmaceuticals, Inc. (US)
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ORIGIN

  Query Match           91.6%;  Score 3721.4;  DB 6;  Length 3900;
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Qy        315 GGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGC 374
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Qy        855 GACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGA 914
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Db        665 GACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGA 724

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Qy       3675 AGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTT 3734
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Db       3485 AGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTT 3544

Qy       3735 CAAGGAGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCC 3794
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Qy       3855 ACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAG 3914
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Db       3665 ACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAG 3724

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Qy       3975 GTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGA 4034
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Db       3785 GTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGA 3844

Qy       4035 AATAAAGCCATTTCAGAGGAAAAAAAA 4061
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RESULT 8
AX402516
LOCUS       AX402516               3599 bp    DNA     linear   PAT 07-JUN-2002
DEFINITION  Sequence 88 from Patent WO0198353.
ACCESSION   AX402516
VERSION     AX402516.1  GI:21387507
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hillman,J.L., Tang,Y.T., Yue,H., Elliott,V.S., Tribouley,C.M.,
            Lee,E.A., Ramkumar,J., Lal,P., Xu,Y., Warren,B.A., Hafalia,A.J.,
            Baughn,M.R., Azimzai,Y., Batra,S., Burford,N., Yao,M.G.,
            Nguyen,D.B., Lu,D.A., Walia,N.K., Au-Young,J. and Patterson,C.
  JOURNAL   Patent: WO 0198353-A 88 27-DEC-2001;
            Incyte Genomics, Inc. (US)
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ORIGIN

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  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3592;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy        449 GGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTG 508
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Db          1 GGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTG 60

Qy        509 CCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATG 568
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Qy        569 TTGGTGTG-GCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCC 627
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Db        121 TTGGTGTGCGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCC 180

Qy        628 ATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGC 687
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Db        181 ATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGC 240

Qy        688 TCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTG 747
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Db        241 TCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTG 300

Qy        748 GACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGC 807
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Db        301 GACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGC 360

Qy        808 GAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGA 867
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Qy        868 GGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTG 927
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Db        421 GGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTG 480

Qy        928 ACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGG 987
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Qy       1048 GCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAG 1107
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Db        601 GCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAG 660

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Db        661 GTCCTTCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCT 720

Qy       1168 TCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGT 1227
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Qy       1228 GGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGC 1287
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Qy      1288 GTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTC 1347
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Qy      1348 GAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATT 1407
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Db       901 GAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATT 960

Qy      1408 TCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGC 1467
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Db       961 TCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGC 1020

Qy      1468 GCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGC 1527
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Db      1021 GCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGC 1080

Qy      1528 ACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCAT 1587
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Db      1081 ACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCAT 1140

Qy      1588 GTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGG 1647
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Db      1141 GTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGG 1200

Qy      1648 GACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACC 1707
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Qy      1768 GCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCA 1827
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Qy      1828 GTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGAC 1887
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Qy       3688 CCCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCC 3747
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RESULT 9
AY046396
LOCUS       AY046396               3701 bp    mRNA    linear   PRI 13-SEP-2001
DEFINITION  Homo sapiens TRP-related cation influx channel (TRPM4) mRNA,
            complete cds.
ACCESSION   AY046396
VERSION     AY046396.1  GI:15617228
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3701)
  AUTHORS   Xu,X.Z., Moebius,F., Gill,D.L. and Montell,C.
  TITLE     Regulation of melastatin, a TRP-related protein, through
            interaction with a cytoplasmic isoform
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (19), 10692-10697 (2001)
  MEDLINE   21438010
   PUBMED   11535825
REFERENCE   2  (bases 1 to 3701)
  AUTHORS   Xu,X.-Z., Moebius,F., Gill,D.L. and Montell,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUL-2001) Biological Chemistry, Johns Hopkins Univ
            School of Medicine, 725 N. Wolfe Street, Baltimore, MD 21205, USA
FEATURES             Location/Qualifiers
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ORIGIN

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Qy        504 GGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCG 563
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RESULT 10
AY297044
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DEFINITION  Homo sapiens transient receptor potential cation channel subfamily
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ACCESSION   AY297044
VERSION     AY297044.1  GI:31335330
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REFERENCE   1  (bases 1 to 3523)
  AUTHORS   Hofmann,T., Chubanov,V., Gudermann,T. and Montell,C.
  TITLE     TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent
            Selective Cation Channel
  JOURNAL   Curr. Biol. 13 (13), 1153-1158 (2003)
  MEDLINE   22726392
   PUBMED   12842017
REFERENCE   2  (bases 1 to 3523)
  AUTHORS   Chubanov,V., Gudermann,T., Hofmann,T. and Montell,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAY-2003) Institut fuer Pharmakologie und
            Toxikologie, Philipps-Universitaet Marburg, Karl-von-Frisch-Strasse
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ORIGIN

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Qy        624 GGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAA 683
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Qy        684 GGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCC 743
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Qy        744 CCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGG 803
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Qy        804 GGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGT 863
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Qy        864 GGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGAT 923
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Qy        984 AGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGG 1043
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Db        608 AGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGG 667

Qy       1044 GGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCT 1103
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Qy       1104 TGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTA 1163
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Qy       1344 TCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCT 1403
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Qy       1404 CATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTA 1463
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Qy       1884 TGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGT 1943
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Qy       1944 TGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCG 2003
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RESULT 11
AX235185
LOCUS       AX235185               3387 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 3 from Patent WO0162794.
ACCESSION   AX235185
VERSION     AX235185.1  GI:15593776
KEYWORDS    .
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Glucksmann,M.A., Curtis,R.A. and Lora,J.M.
  TITLE     18607, a human calcium channel
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            Millennium Pharmaceuticals, Inc. (US)
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ORIGIN

  Query Match           83.1%;  Score 3373.8;  DB 6;  Length 3387;
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Db       1091 TCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCCT 1150
Qy       1478 CCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCCC 1537
Db       1151 CCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCCC 1210
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Db       1211 CAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGGA 1270
Qy       1598 TGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACC 1657
Db       1271 TGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACC 1330
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Db       1331 CAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCT 1390
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Db       1391 CGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGC 1450
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Qy       1898 CAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCG 1957
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Qy       2198 CCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTG 2257
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Qy       2438 GCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGC 2497
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Qy       2498 CGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAAC 2557
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Qy       2558 TGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCC 2617
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Qy       2618 ATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACC 2677
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Qy       2978 GTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGG 3037
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Qy       3038 AGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGG 3097
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Qy       3338 TCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATT 3397
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Qy       3458 AGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGA 3517
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Db       3131 AGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGA 3190

Qy       3518 AGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACG 3577
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Db       3191 AGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACG 3250

Qy       3578 AACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGG 3637
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Qy       3638 TGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACC 3697
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Qy       3698 TGCCTGGGTCCAAAGAC 3714
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RESULT 12
CQ715325
LOCUS       CQ715325               3402 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 1259 from Patent WO02068579.
ACCESSION   CQ715325
VERSION     CQ715325.1  GI:42276182
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 1259 06-SEP-2002;
            PE Corporation (NY) (US)
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
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  Query Match             82.1%;  Score 3336;  DB 6;  Length 3402;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3339;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        374 CAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAG 433
              ||| |   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         59 CAGATCCGGGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAG 118

Qy        434 TGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTG 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 TGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTG 178

Qy        494 GGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGG 553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 GGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGG 238

Qy        554 GCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCA 613
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Db        239 GCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCA 298

Qy        614 CCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCA 673
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Qy        674 TCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGG 733
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Db        359 TCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGG 418

Qy        734 TCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACG 793
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Db        419 TCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACG 478

Qy        794 GCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGA 853
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Qy        914 ATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCG 973
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Db        599 ATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCG 658

Qy        974 TGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCC 1033
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Db        659 TGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCC 718

Qy       1034 CAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCA 1093
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Db        719 CAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCA 778

Qy       1094 AAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCC 1153
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Db        779 AAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCC 838

Qy       1154 TGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCC 1213
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Db        839 TGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCC 898

Qy       1214 TTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTG 1273
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Db        899 TTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTG 958

Qy       1274 TGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGC 1333
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Qy       1334 GGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCG 1393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1019 GGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCG 1078
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Qy      1394 TGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGG 1453
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Qy      1694 CGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCG 1753
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Qy      1814 TGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCAC 1873
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Qy      1874 GCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGG 1933
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Db      1559 GCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGG 1618

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Db      1619 GGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCC 1678

Qy      1994 TCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAG 2053
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Qy      3074 CACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGG 3133
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Db      2759 CACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGG 2818

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RESULT 13
AY297046
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DEFINITION  Homo sapiens transient receptor potential cation channel subfamily
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ACCESSION   AY297046
VERSION     AY297046.1  GI:31335334
KEYWORDS    .
SOURCE      Homo sapiens (human)
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REFERENCE   1  (bases 1 to 3444)
  AUTHORS   Hofmann,T., Chubanov,V., Gudermann,T. and Montell,C.
  TITLE     TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent
            Selective Cation Channel
  JOURNAL   Curr. Biol. 13 (13), 1153-1158 (2003)
  MEDLINE   22726392
   PUBMED   12842017
REFERENCE   2  (bases 1 to 3444)
  AUTHORS   Chubanov,V., Hofmann,T., Gudermann,T. and Montell,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAY-2003) Institut fuer Pharmakologie und
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ORIGIN

  Query Match             73.8%;  Score 2999;  DB 9;  Length 3444;
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  Matches 3444;  Conservative    0;  Mismatches    0;  Indels  435;  Gaps    1;

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Qy        381 TAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGG 440
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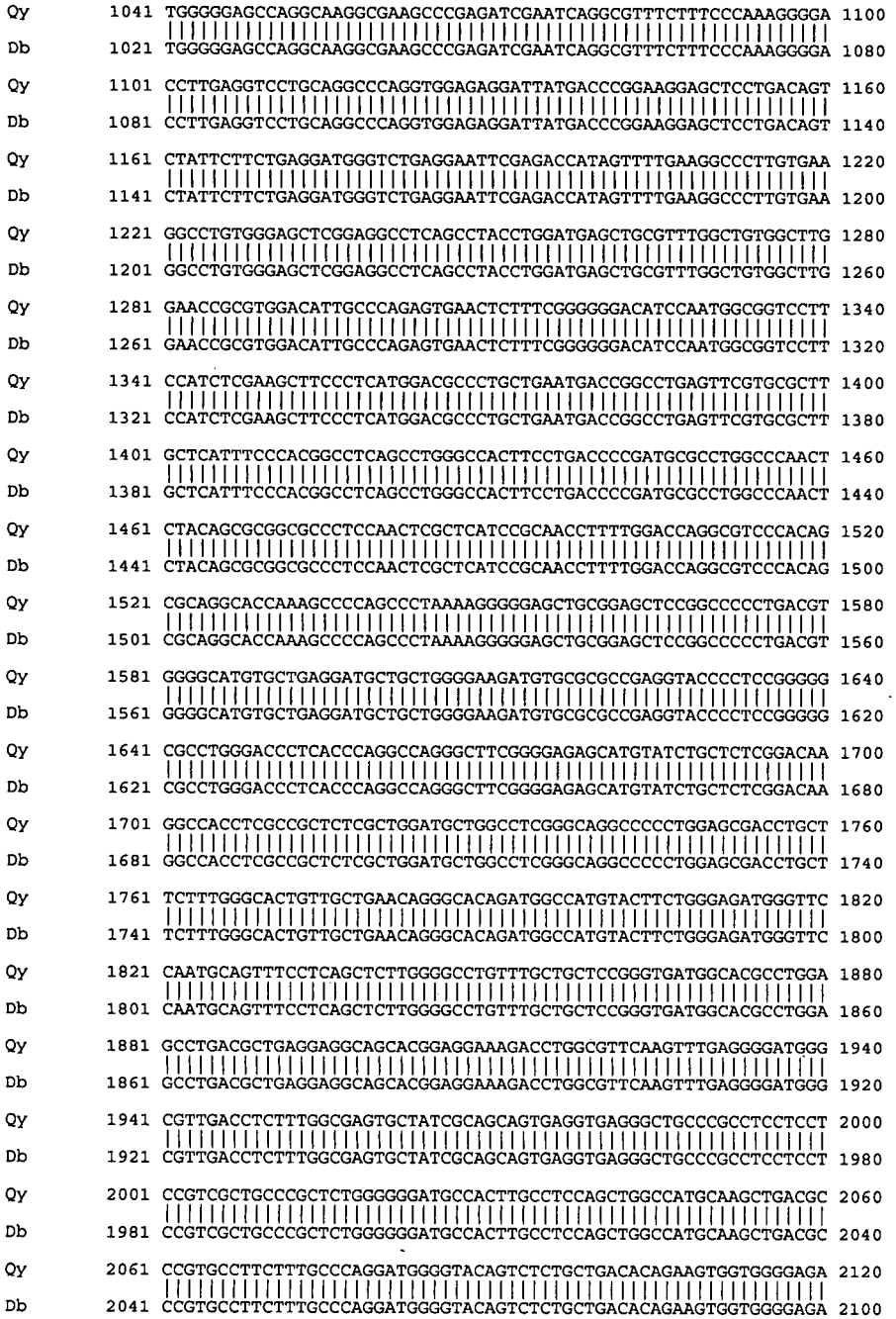
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RESULT 14
AX443225
LOCUS       AX443225               2695 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 7 from Patent WO0210382.
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VERSION     AX443225.1  GI:21690620
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REFERENCE   1
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  TITLE     Trp8, trp9 and trp10, markers for cancer
  JOURNAL   Patent: WO 0210382-A 7 07-FEB-2002;
            Wissenbach, Ulrich (DE)
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ORIGIN

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DEFINITION  Homo sapiens cDNA FLJ20228 fis, clone COLF5163.
ACCESSION   AK000235
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,
            Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
            Nakamura,Y., Isogai,T. and Sugano,S.
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  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2981)
  AUTHORS   Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
            Shibahara,T., Tanaka,T. and Nakamura,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,
            University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1,
            Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp,
            Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            International Trade and Industry of Japan; cDNA full insert
            sequencing: Research Association for Biotechnology; cDNA library
            construction, 5'- & 3'-end one pass sequencing: Departent of
            Virology and Human Genome Center, Institute of Medical Science,
            University of Tokyo (partly supported by Science and Technology
            Agency).
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ORIGIN

  Query Match             62.6%;  Score 2543.8;  DB 9;  Length 2981;
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Db       1547 CGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTG 1606

Qy       2715 CCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGT 2774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1607 CCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGT 1666

Qy       2775 TTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGT 2834
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Db       1667 TTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGT 1726

Qy       2835 CATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCT 2894
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1727 CATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCT 1786

Qy       2895 GGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAG 2954
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1787 GGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAG 1846

Qy       2955 TATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGA 3014
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1847 TATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGA 1906

Qy       3015 GGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGC 3074
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1907 GGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGC 1966

Qy       3075 ACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGT 3134
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1967 ACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGT 2026

Qy       3135 GCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGC 3194
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2027 GCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGC 2086

Qy       3195 CATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCA 3254
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2087 CATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCA 2146

Qy       3255 GCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGT 3314
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2147 GCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGT 2206

Qy       3315 CATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCC 3374
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2207 CATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCC 2266

Qy       3375 GTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCT 3434
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Db       2267 GTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCT 2326

Qy       3435 GCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCG 3494
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Db       2327 GCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCG 2386

Qy       3495 GGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACA 3554
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Db       2387 GGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACA 2446

Qy       3555 GCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCA 3614
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Db       2447 GCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCA 2506

Qy       3615 GTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCC 3674
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Db       2507 GTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCC 2566

Qy       3675 AGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTT 3734
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2567 AGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTT 2626

Qy       3735 CAAGGAGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCC 3794
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2627 CAAGGAGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCC 2686

Qy       3795 CCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGG 3854
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Db       2687 CCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGG 2746

Qy       3855 ACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAG 3914
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2747 ACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAG 2806

Qy       3915 TCCCAGCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGG 3974
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2807 TCCCAGCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGG 2866

Qy       3975 GTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGA 4034
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2867 GTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGA 2926

Qy       4035 AATAAAGCCATTTCAGAGGAAAAAAAA 4061
             ||||||||||||||||||||||||||||
Db       2927 AATAAAGCCATTTCAGAGGAAAAAAAA 2953
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Search completed: June 13, 2005, 02:43:38
Job time : 11459.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 04:57:16 ; Search time 1356.41 Seconds
(without alignments)
17723.358 Million cell updates/sec

Title: US-09-869-486B-29
Perfect score: 4061
Sequence: 1 ggtctggaagcagagccggc.....ccatttcagaggaaaaaaaa 4061

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4061	100.0	4061	3	AAA49923	Aaa49923 Human cal
2	4061	100.0	4061	10	ADH62711	Adh62711 Ca activa
3	4061	100.0	4061	13	ADR73511	Adr73511 Human TRP
4	4061	100.0	4061	13	ADS12774	Ads12774 Transient
5	4028.4	99.2	4042	6	AAD32372	Aad32372 Human Trp
6	3845	94.7	4641	11	ADN39239	Adn39239 Cancer/an
7	3812.2	93.9	3898	12	ADL06463	Adl06463 Human tum
8	3759.6	92.6	3810	6	ABK92167	Abk92167 Prostate
9	3759.6	92.6	3810	13	ADR66772	Adr66772 Human pro
10	3759.6	92.6	3810	13	ADR65869	Adr65869 Human pro
11	3759.6	92.6	3810	13	ADS12778	Ads12778 Human TRP
12	3721.4	91.6	3900	5	AAH76383	Aah76383 Human TLC
13	3721.4	91.6	3900	8	ABS58041	Abs58041 Human tra
14	3721.4	91.6	3900	12	ADH51622	Adh51622 Human 186
15	3579.8	88.2	3599	6	ABK28677	Abk28677 Human cDN
16	3542	87.2	3701	13	ADS12776	Ads12776 Transient
17	3538.8	87.1	3676	12	ADQ83682	Adq83682 Human tum
18	3538.8	87.1	3676	13	ADQ85834	Adq85834 Human tum
19	3538.8	87.1	3676	13	ADQ86998	Adq86998 Human tum
20	3501	86.2	3501	6	ABK92224	Abk92224 Prostate
21	3501	86.2	3501	11	ADN39597	Adn39597 Cancer/an
22	3399	83.7	3583	11	ADL33391	Adl33391 Human tra
23	3376.8	83.2	3390	12	ADH51624	Adh51624 Human 186
24	3373.8	83.1	3387	5	AAH76384	Aah76384 Human TLC
25	2616.4	64.4	2695	6	AAD32373	Aad32373 Human Trp
26	2412.4	59.4	2459	12	ADL06424	Adl06424 Human tum
27	2258	55.6	2393	2	AAV26656	Aav26656 Human PS1
28	2258	55.6	2393	3	AAA64090	Aaa64090 Consensus
29	1978.8	48.7	2180	3	AAA49921	Aaa49921 Human cal
30	1505	37.1	1524	2	AAV58585	Aav58585 Prostate
31	1505	37.1	1524	2	AAV61200	Aav61200 Full leng
32	1505	37.1	1524	3	AAA06348	Aaa06348 Human imm
33	1505	37.1	1524	3	ABS71253	Abs71253 Human pro
34	1505	37.1	1524	4	AAH93464	Aah93464 Human pro
35	1505	37.1	1524	4	AAS63556	Aas63556 Human pro
36	1505	37.1	1524	4	AAH02529	Aah02529 Prostate
37	1505	37.1	1524	4	AAH84778	Aah84778 Human pro
38	1505	37.1	1524	5	ACA59365	Aca59365 Prostate
39	1505	37.1	1524	5	AAS10107	Aas10107 Human pro
40	1505	37.1	1524	6	ABL94928	Abl94928 Human J1-
41	1505	37.1	1524	6	ABS58637	Abs58637 Prostate
42	1505	37.1	1524	8	ACC95092	Acc95092 Prostate
43	1505	37.1	1524	10	ADB13559	Adb13559 Human pro
44	1505	37.1	1524	10	ADG25975	Adg25975 Human pro
45	1505	37.1	1524	12	ADL06460	Adl06460 Human tum

ALIGNMENTS

RESULT 1
AAA49923
ID AAA49923 standard; cDNA; 4061 BP.
XX
AC AAA49923;
XX
DT 10-OCT-2000 (first entry)
XX
DE Human calcium channel SOC-3/CRAC-2 cDNA.
XX
KW SOC-2/CRAC-1; calcium channel; human; store operated channel;
KW calcium release activated channel; therapy; diagnosis;
KW lymphocyte proliferative disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 382. .5979
FT /*tag= a
XX
PN WO200040614-A2.
XX
PD 13-JUL-2000.
XX
PF 20-DEC-1999; 99WO-US029996.
XX
PR 30-DEC-1998; 98US-0114220P.
PR 29-JAN-1999; 99US-0120018P.
PR 22-JUN-1999; 99US-0140415P.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Scharenberg AM;
XX
DR WPI; 2000-465957/40.
DR P-PSDB; AAY95436.
XX
PT New SOC/CRAC calcium channel polynucleotides and polypeptides used to
PT diagnose and treat proliferative disorders associated with the channel,
PT and to screen for novel modulators of the channel.
XX
PS Claim 1(a); Page 99-100; 108pp; English.
XX

CC The present sequence is a full-length nucleotide sequence of human SOC-
CC 3/CRAC-2 cDNA. It includes an open reading frame encoding SOC-3/CRAC-2
CC (see AAY95436), a member of a novel family of store operated channel
CC (SOC) or calcium release activated channel (CRAC) polypeptides that
CC modulate Ca2+ flux into and out of a cell, and which may be activated
CC upon depletion of Ca2+ from intracellular calcium stores, allowing Ca2+
CC influx into a cell. SOC-3/CRAC-2 is expressed predominantly in kidney and
CC colon. Compositions for expressing SOC/CRAC calcium channel polypeptides
CC in cells may be useful for treating patients that have reduced
CC extracellular calcium influx into their SOC/CRAC-expressing cells. They
CC will also be useful for delivering therapeutic and/or imaging agents to
CC such cells to modulate proliferation and growth. SOC/CRAC polypeptides
CC also represent targets for designing and/or identifying inhibitors that
CC block lymphocyte proliferation and binding agents that selectively bind
CC to SOC/CRAC polypeptides to which drugs or toxins can be conjugated for
CC delivery to SOC/CRAC expressing cells. SOC/CRAC polynucleotides are used
CC as probes and primers to identify other members of the SOC/CRAC family of
CC calcium channels, as diagnostic reagents for identifying the presence of
CC SOC/CRAC polypeptides in biological samples, as agents for generating
CC SOC/CRAC binding polypeptides, and in gene therapy. Methods for
CC determining the level of SOC/CRAC expression in a subject can be used to
CC assess the presence, or absence, or stage of a proliferative disorder,
CC e.g. a lymphocyte proliferative disorder
XX
SQ Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

Query Match 100.0%; Score 4061; DB 3; Length 4061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGTCTGGAAGCAGAGCCGGCGGAGGGAGCGCCGGGGCCCTGGGCTGCAGGAGGTTGCGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTCTGGAAGCAGAGCCGGCGGAGGGAGCGCCGGGGCCCTGGGCTGCAGGAGGTTGCGGC 60

Qy         61 GGCCGCGGCAGCATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCCGCGGCAGCATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAG 120

Qy        121 AAGAAGACCTGCACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGAAGACCTGCACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAG 180

Qy        181 TGTGGGCGCCCCCGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGGGCGCCCCCGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCC 240

Qy        241 GTGGTGACCGTGTGGGACAGCGATGCACACACCACGGAGAAGCCCACCGATGCCTACGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGTGACCGTGTGGGACAGCGATGCACACACCACGGAGAAGCCCACCGATGCCTACGGA 300

Qy        301 GAGCTGGACTTCACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGCTGGACTTCACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGA 360

Qy        361 ACGGATCCAGCTGCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACGGATCCAGCTGCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAAC 420

Qy        421 CTGGTGGTGTCAGTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGTGGTGTCAGTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGAC 480

Qy        481 CTGCTGCGTCGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGCTGCGTCGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGG 540

Qy        541 GGTCTGCACACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGTCTGCACACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCC 600

Qy        601 AGCACTGGGGGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCACTGGGGGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAAT 660

Qy        661 AGAGACACCCTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGAGACACCCTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGAC 720

Qy        721 CCGGAGGACGGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCGGAGGACGGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGAC 780

Qy        781 GACGGCACACACGGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACGGCACACACGGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTAC 840

Qy        841 ATCTCACAGCAGAAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATCTCACAGCAGAAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTC 900

Qy        901 CTGATTGATGGTGATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGATTGATGGTGATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTC 960

Qy        961 CCATGTCTCCTCGTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCATGTCTCCTCGTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAA 1020

Qy       1021 GACACTCTGGCCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GACACTCTGGCCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGG 1080

Qy       1081 CGTTTCTTTCCCAAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACC 1140
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Db       1081 CGTTTCTTTCCCAAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACC 1140

Qy       1141 CGGAAGGAGCTCCTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CGGAAGGAGCTCCTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATA 1200

Qy       1201 GTTTTGAAGGCCCTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GTTTTGAAGGCCCTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAG 1260

Qy       1261 CTGCGTTTGGCTGTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTGCGTTTGGCTGTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGG 1320

Qy       1321 GACATCCAATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GACATCCAATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGAC 1380

Qy       1381 CGGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACC 1440

Qy       1441 CCGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTT 1500

Qy       1501 TTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCG 1560

Qy       1561 GAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCG 1620

Qy       1621 CCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGC 1680

Qy       1681 ATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAG 1740
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Qy       1741 GCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATG 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATG 1800

Qy       1801 TACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTC 1860
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Qy       2041 CTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTG 2100
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Qy       2221 CCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTC 2280
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Db       2221 CCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTC 2280

Qy       2281 GGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCG 2340
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Qy       2341 GGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGG 2400
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Qy       2401 GGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTT 2460
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Db       4021 CCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAAAAAAA 4061


RESULT 2
ADH62711
ID   ADH62711 standard; cDNA; 4061 BP.
XX
AC   ADH62711;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Ca activated nonselective transmembrane channel protein TRPM4b cDNA.
XX
KW   bioactive agent; monovalent cation permeability; TRPM4b channel; human;
KW   calcium activated nonselective transmembrane channel; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             73. .3717
FT                   /*tag=  a
FT                   /product= "TRPM4b"
FT                   /note= "Calcium activated nonselective (CAN)
FT                   transmembrane channel protein"
XX
PN   US2003143557-A1.
XX
PD   31-JUL-2003.
XX
PF   08-MAY-2002; 2002US-00142649.
XX
PR   25-JAN-2002; 2002US-0351938P.
PR   02-MAY-2002; 2002US-0377937P.
XX
PA   (PENN/) PENNER R.
XX
PI   Penner R;
XX
DR   WPI; 2003-829785/77.
DR   P-PSDB; ADH62712.
XX
PT   Screening for candidate bioactive agents involves contacting calcium-
PT   activated nonselective transmembrane channel polypeptide designated as
PT   TRPM4b with candidate agent, determining binding of candidate agent
PT   TRPM4b.
XX
PS   Claim 5; SEQ ID NO 1; 25pp; English.
XX
CC   The invention describes a method of screening (M1) for a candidate
CC   bioactive agent (CA) modulating monovalent cation (MC) permeability of
CC   the TRPM4b (I) channel. The method involves providing a recombinant cell
CC   (RC) with a nucleic acid encoding (I) and an inducible promoter operably
CC   linked to (I), capable of expressing (I), and comprises an MC indicator,
CC   inducing RC to express (I), contacting RC with MC and CA, and detecting
CC   intracellular levels of MC with an indicator. The method is useful for
CC   creening for a candidate bioactive agent capable of modulating monovalent
CC   cation permeability of a TRPM4b channel. This sequence encodes human
CC   calcium activated nonselective (CAN) transmembrane channel protein
CC   TRPM4b.
XX
SQ   Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 4061;  DB 10;  Length 4061;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 4061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTCTGGAAGCAGAGCCGGCGGAGGGAGCGCCGGGGCCCTGGGCTGCAGGAGGTTGCGGC 60
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Qy        541 GGTCTGCACACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCC 600
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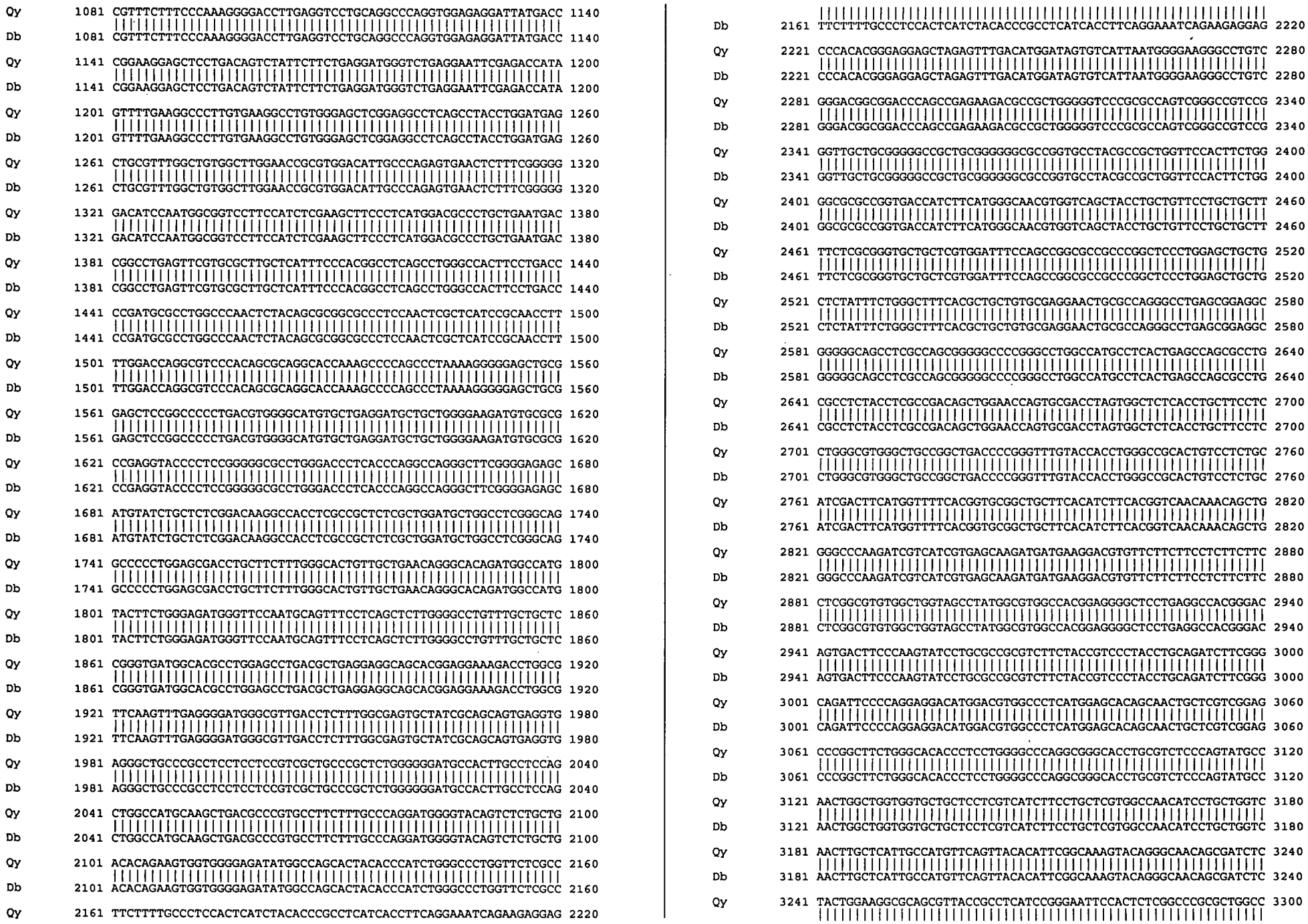
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Qy 2401 GGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTT 2460
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Qy 2581 GGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTG 2640
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Qy 2701 CTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGC 2760
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Qy       3361 CGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAA 3420
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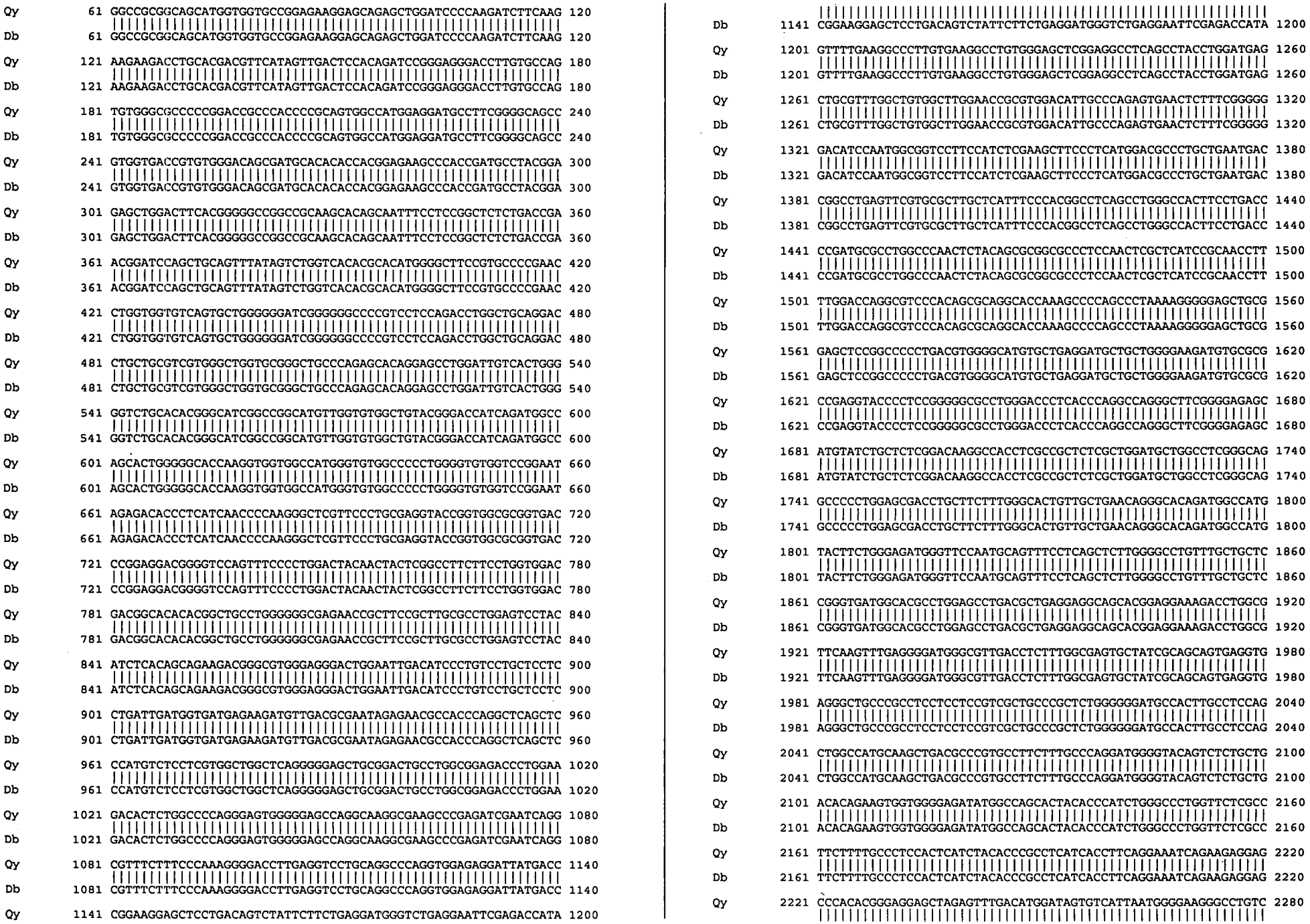
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             |||||||||||||||||||||||||||||||||||||||||
Db       4021 CCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAAAAAAA 4061


RESULT 3
ADR73511
ID   ADR73511 standard; DNA; 4061 BP.
XX
AC   ADR73511;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human TRPM4, gene.
XX
KW   TRPM4; apoptosis; inhibitor; tumour; cytostatic; cancer; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             73. .3717
FT                   /*tag=  a
FT                   /product= "Human TRPM4"
XX
PN   WO2004076682-A2.
XX
PD   10-SEP-2004.
XX
PF   26-FEB-2004; 2004WO-US006020.
XX
PR   26-FEB-2003; 2003US-0450886P.
XX
PA   (SURR-) SURROMED INC.
XX
PI   Axenovich SA,  Stull R,  Gelman M,  Chui K,  Ng D;
XX
DR   WPI; 2004-653428/63.
DR   P-PSDB; ADR73512.
XX
PT   Identifying a compound for inducing apoptosis, useful for diagnosing and
PT   treating cancer, comprises identifying an inhibitor of a target.
XX
PS   Example 1; SEQ ID NO 79; 255pp; English.
XX
CC   The invention relates to a novel method for identifying a compound for
CC   inducing apoptosis comprises identifying an inhibitor of a target.
CC   Examples of an inhibitor of a target include: angio-associated, migratory
CC   cell protein (AAMP), disintegrin and metalloproteinase domain 8 (ADAM8),
CC   disintegrin-like and metalloprotease (reporlysin type) with
CC   thrombospondin type 1 motif, 17 (ADAMTS17), adenylate cyclase 3 (ADCY3),
CC   adrenergic beta receptor kinase 1 (ADRBK1), bladder cancer associated
CC   protein (BLCAP), chromosome 22 open reading frame 5 (C22orf5), CD81
CC   antigen (target of antiproliferative antibody 1 (CD81), CD9 antigen (p24)
CC   (CD9), claudin 4 (CLDN4), chloride intracellular channel 1 (CLIC1),
CC   collagen, type VI, alpha 2 (COL6A2), CTL2, endothelin converting enzyme 1
CC   (ECE1), ephrinB1 (EFNB1), flotillin 2 (FLOT2), intercellular adhesion
CC   molecule 3 (ICAM3), iduronate 2-sulfatase (Hunter syndrome) (IDS), jagged
CC   2 (JAG2), junctional adhesion molecule 1 (JAM1), lectin, galactoside-
CC   binding soluble 3 binding protein (LGALS3BP), similar to possible G-
CC   protein receptor (LOC146330), CGI-78 protein (LOC51107), lipoprotein
CC   lipase (LPL), low density lipoprotein receptor-related protein 5 (LRP5),
CC   Lutheran blood group (Auberger b antigen included) (LU), membrane
CC   component, chromosome11, surface marker 1 (M11S1), serum constituent
CC   protein (MSE55), neuropathy target esterase (NTE), Homo sapiens cDNA
CC   FL31043 fis, clone HSYRA2000248 (PLEXIN A1) or Homo sapiens cDNA FLJ44113
CC   fis, clone TESTI4046487, highly similar to Mus musculus plexin A1
CC   (PLXNA1), protein tyrosine phosphatase, receptor type, f polypeptide
CC   (PTPRF), interacting protein) (liprin), alpha 3 (PPFIA3), Homo sapiens
CC   peptide-histidine transporter 4 (PTR4), mRNA (PTR4), solute carrier
CC   family 16 (monocarboxylic acid transporters) member 3 (SLC16A3), solute
CC   carrier family 1 (neutral amino acid transporter) member 5 (SLC1A5),
CC   solute carrier family 39 (zinc transporter) member 3 (SLC39A1), serine
CC   protease inhibitor, Kunitz type 2 (SPINT2), stanniocalcin 2 (STC2),
CC   tumour necrosis receptor superfamily member 21 (TNFRSF21), tumour
CC   rejection antigen (gp96) 1 (TRA1), or transient receptor potential cation
CC   channel, subfamily M member 4 (TRPM4), respectively comprising any of the
CC   40 sequences of 87-1615 amino acids (the even numbers selected from SEQ
CC   ID:2-80), shown in the specification. The invention further comprises a
CC   method for inducing apoptosis and a method for diagnosing a tumour. The
CC   novel compounds have cytostatic activity. The method is useful for
CC   identifying a compound for inducing apoptosis. The methods and compounds
CC   are useful for diagnosing and treating cancer, and in determining the
CC   prognosis for cancer in the patient or the susceptibility of the patient
CC   to a therapeutic treatment. This polynucleotide sequence represents a
CC   gene encoding one of the 40 protein targets of the invention.
XX
SQ   Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 4061;  DB 13;  Length 4061;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 4061;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTCTGGAAGCAGAGCCGGCGGAGGGAGCGCCGGGGCCCTGGGCTGCAGGAGGTTGCGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTCTGGAAGCAGAGCCGGCGGAGGGAGCGCCGGGGCCCTGGGCTGCAGGAGGTTGCGGC 60
```


Qy 61 GGCCGCGGCAGCATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAG 120
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Qy 121 AAGAAGACCTGCACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAG 180
Db 121 AAGAAGACCTGCACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAG 180
Qy 181 TGTGGGCGCCCCCGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCC 240
Db 181 TGTGGGCGCCCCCGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCC 240
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Qy 481 CTGCTGCGTCGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGG 540
Db 481 CTGCTGCGTCGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGG 540
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Qy 601 AGCACTGGGGGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAAT 660
Db 601 AGCACTGGGGGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAAT 660
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Qy       2581 GGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTG 2640
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Qy       3241 TACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCC 3300
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Qy       3361 CGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAA 3420
Db       3361 CGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAA 3420
Qy       3421 GCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGC 3480
Db       3421 GCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGC 3480
Qy       3481 GCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGAC 3540
Db       3481 GCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGAC 3540
Qy       3541 TTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAG 3600
Db       3541 TTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAG 3600
Qy       3601 CGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCT 3660
Db       3601 CGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCT 3660
Qy       3661 GCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCC 3720
Db       3661 GCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCC 3720
Qy       3721 CTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCA 3780
Db       3721 CTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCA 3780
Qy       3781 TCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCT 3840
Db       3781 TCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCT 3840
Qy       3841 GGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCT 3900
Db       3841 GGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCT 3900
Qy       3901 CCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTTATCCAT 3960
Db       3901 CCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTTATCCAT 3960
Qy       3961 CTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATT 4020
Db       3961 CTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATT 4020
Qy       4021 CCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAAAAAAA 4061
Db       4021 CCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAAAAAAA 4061
```

RESULT 4
ADS12774
ID ADS12774 standard; cDNA; 4061 BP.
XX
AC ADS12774;
XX
DT 16-DEC-2004 (first entry)
XX
DE Transient receptor potential cation channel, subfamily M member 4b cDNA.
XX
KW transient receptor potential cation channel; subfamily M; member 4;
KW TRPM4; phospholipase A1-A; PLA1A; butyryl coenzyme A synthetase 1; BUCS1;
KW prostate cancer; TRPM4b; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   73. .3717
FT   /*tag= a
FT   /product= "Human TRPM4b protein"
XX
PN JP2004267118-A.
XX

PD 30-SEP-2004.
XX
PF 10-MAR-2003; 2003JP-00063578.
XX
PR 10-MAR-2003; 2003JP-00063578.
XX
PA (SANY) SANKYO CO LTD.
XX
DR WPI; 2004-693915/68.
DR P-PSDB; ADS12775.
XX
PT Detecting prostatic cancer, comprises extracting RNA fractions from test
PT substance of subject and normal human, measuring and analyzing the
PT difference in e.g., phospholipase A1-A and butyryl coenzyme A synthetase
PT expression levels.
XX
PS Claim 1; SEQ ID NO 1; 126pp; Japanese.
XX
CC The invention comprises a method for detecting prostatic cancer in a
CC subject. The method involves measuring the expression levels of specific
CC genes: transient receptor potential cation channel, subfamily M, member 4
CC (TRPM4); phospholipase A1-A (PLA1A); and butyryl coenzyme A synthetase 1
CC (BUCS1). The method of the invention is useful for the detection and
CC treatment of prostate cancer. The present cDNA sequence encodes the human
CC TRPM4b protein of the invention.
XX
SQ Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

Query Match 100.0%; Score 4061; DB 13; Length 4061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGTCTGGAAGCAGAGCCGGCGGAGGGAGCGCCGGGGCCCTGGGCTGCAGGAGGTTGCGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTCTGGAAGCAGAGCCGGCGGAGGGAGCGCCGGGGCCCTGGGCTGCAGGAGGTTGCGGC 60

Qy         61 GGCCGCGGCAGCATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCCGCGGCAGCATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAG 120

Qy        121 AAGAAGACCTGCACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGAAGACCTGCACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAG 180

Qy        181 TGTGGGCGCCCCCGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGGGCGCCCCCGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCC 240

Qy        241 GTGGTGACCGTGTGGGACAGCGATGCACACACCACGGAGAAGCCCACCGATGCCTACGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGTGACCGTGTGGGACAGCGATGCACACACCACGGAGAAGCCCACCGATGCCTACGGA 300

Qy        301 GAGCTGGACTTCACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGCTGGACTTCACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGA 360

Qy        361 ACGGATCCAGCTGCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACGGATCCAGCTGCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAAC 420

Qy        421 CTGGTGGTGTCAGTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGTGGTGTCAGTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGAC 480

Qy        481 CTGCTGCGTCGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGCTGCGTCGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGG 540

Qy        541 GGTCTGCACACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGTCTGCACACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCC 600

Qy        601 AGCACTGGGGGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCACTGGGGGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAAT 660

Qy        661 AGAGACACCCTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGAGACACCCTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGAC 720

Qy        721 CCGGAGGACGGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCGGAGGACGGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGAC 780

Qy        781 GACGGCACACACGGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACGGCACACACGGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTAC 840

Qy        841 ATCTCACAGCAGAAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATCTCACAGCAGAAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTC 900

Qy        901 CTGATTGATGGTGATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGATTGATGGTGATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTC 960

Qy        961 CCATGTCTCCTCGTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCATGTCTCCTCGTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAA 1020

Qy       1021 GACACTCTGGCCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GACACTCTGGCCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGG 1080

Qy       1081 CGTTTCTTTCCCAAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CGTTTCTTTCCCAAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACC 1140

Qy       1141 CGGAAGGAGCTCCTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CGGAAGGAGCTCCTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATA 1200

Qy       1201 GTTTTGAAGGCCCTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GTTTTGAAGGCCCTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAG 1260

Qy       1261 CTGCGTTTGGCTGTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTGCGTTTGGCTGTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGG 1320

Qy       1321 GACATCCAATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GACATCCAATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGAC 1380

Qy       1381 CGGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACC 1440

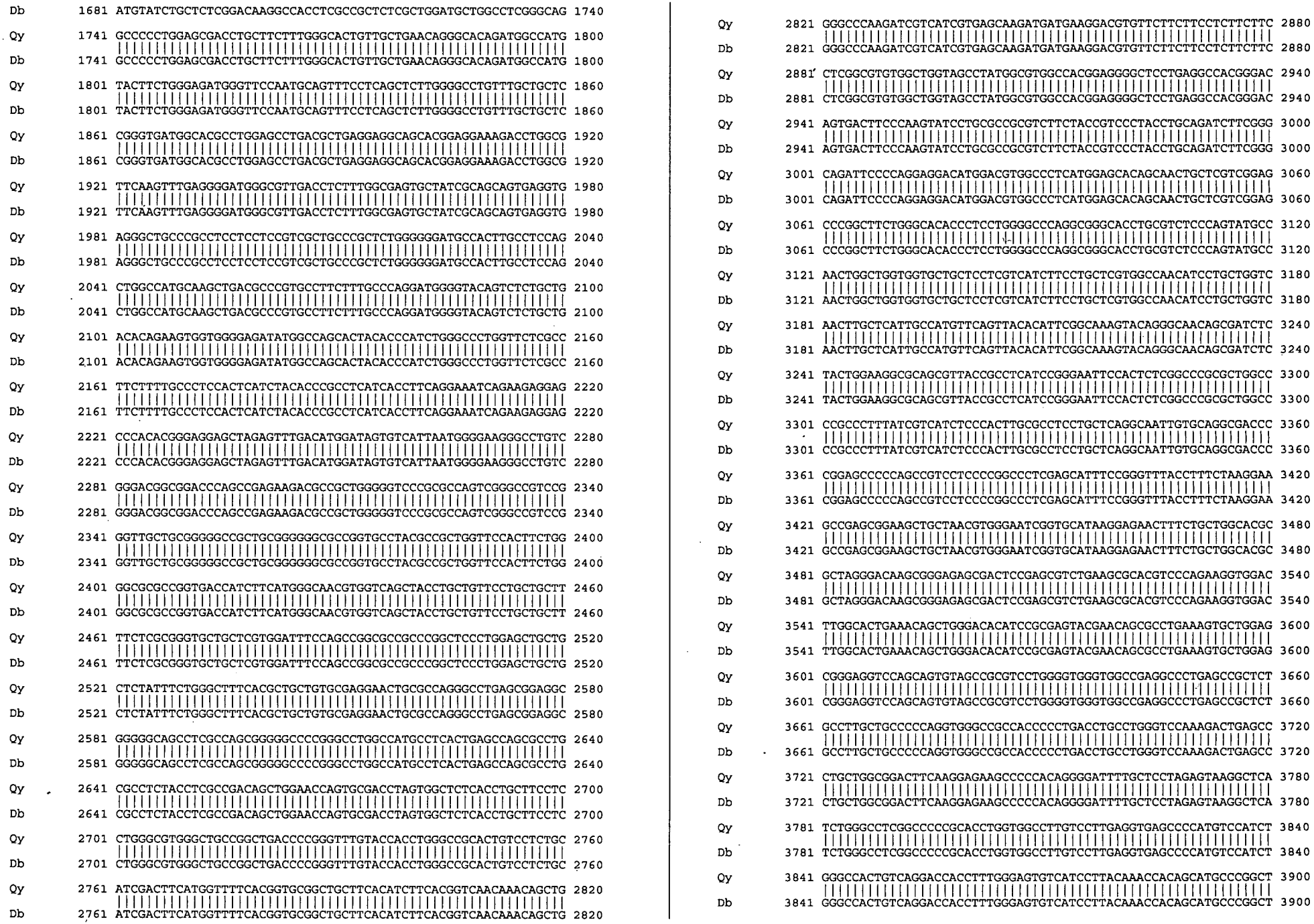
Qy       1441 CCGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1501 TTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1561 GAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCG 1620

Qy       1621 CCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGC 1680

Qy       1681 ATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 1681 ATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAG 1740
Qy 1741 GCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATG 1800
Db 1741 GCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATG 1800
Qy 1801 TACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTC 1860
Db 1801 TACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTC 1860
Qy 1861 CGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCG 1920
Db 1861 CGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCG 1920
Qy 1921 TTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTG 1980
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Qy 1981 AGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAG 2040
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Qy 2101 ACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCC 2160
Db 2101 ACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCC 2160
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Qy 2221 CCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTC 2280
Db 2221 CCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTC 2280
Qy 2281 GGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCG 2340
Db 2281 GGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCG 2340
Qy 2341 GGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGG 2400
Db 2341 GGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGG 2400
Qy 2401 GGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTT 2460
Db 2401 GGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTT 2460
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Qy 2581 GGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTG 2640
Db 2581 GGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTG 2640
Qy 2641 CGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTC 2700
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Qy 2701 CTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGC 2760
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Qy 2761 ATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTG 2820
Db 2761 ATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTG 2820
Qy 2821 GGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTC 2880
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Qy 2881 CTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGAC 2940
Db 2881 CTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGAC 2940
Qy 2941 AGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGG 3000
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Qy 3181 AACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTC 3240
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Db 3601 CGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCT 3660
Qy 3661 GCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCC 3720
Db 3661 GCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCC 3720
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Db 3721 CTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCA 3780
Qy 3781 TCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCT 3840
Db 3781 TCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCT 3840
Qy 3841 GGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCT 3900
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```
Qy       3901 CCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTTATCCAT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3961 CTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATT 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 CTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATT 4020

Qy       4021 CCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAAAAAAA 4061
             |||||||||||||||||||||||||||||||||||||||||
Db       4021 CCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAAAAAAA 4061


RESULT 5
AAD32372
ID   AAD32372 standard; cDNA; 4042 BP.
XX
AC   AAD32372;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human Trp9 protein encoding cDNA.
XX
KW   Human; prostate carcinoma associated protein; Trp9; Trp10a; Trp10b;
KW   transient receptor potential; calcium channel protein; Trp8a; Trp8b;
KW   molecular marker; endometrial cancer; uterine carcinoma; melanoma; gene;
KW   tumour; chorion carcinoma; lung cancer; antisense therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             42. .3686
FT                   /*tag=  a
FT                   /product= "Human Trp9 protein"
XX
PN   WO200210382-A2.
XX
PD   07-FEB-2002.
XX
PF   18-JUL-2001; 2001WO-EP008309.
XX
PR   28-JUL-2000; 2000US-0221513P.
XX
PA   (WISS/) WISSENBACH U.
XX
PI   Wissenbach U;
XX
DR   WPI; 2002-269013/31.
DR   P-PSDB; AAE20283.
XX
PT   Novel isolated nucleic acid encoding human prostate carcinoma associated
PT   protein such as transient receptor potential 8a, 8b, 10a, 10b proteins,
PT   useful as molecular markers for diagnosing prostate cancer.
XX
PS   Claim 1; Fig 9A; 70pp; English.
XX
CC   The invention relates to human prostate carcinoma associated proteins
CC   such as transient receptor potential (Trp)8a, Trp8b, Trp9, Trp10a and
CC   Trp10b and nucleic acid molecules encoding such polypeptides. Trp8, Trp9,
CC   Trp10 are novel calcium channel proteins. Sequences of the invention are
CC   useful as molecular markers for diagnosing prostate cancer. Sequences of
CC   the invention, their antibodies, inhibitors and antisense molecules are
CC   useful for preventing, treating or ameliorating a prostate tumour,
CC   endometrial cancer (uterine carcinoma), tumour, a chorion carcinoma,
CC   cancer of the lung or melanoma. Polynucleotides of the invention are used
CC   in antisense therapy. The present sequence is human Trp9 protein encoding
CC   cDNA
XX
SQ   Sequence 4042 BP; 703 A; 1260 C; 1290 G; 789 T; 0 U; 0 Other;

  Query Match             99.2%;  Score 4028.4;  DB 6;  Length 4042;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4029;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy         32 CGGGGCCCTGGGCTGCAGGAGGTTGCGGCGGCCGCGGCAGCATGGTGGTGCCGGAGAAGG 91
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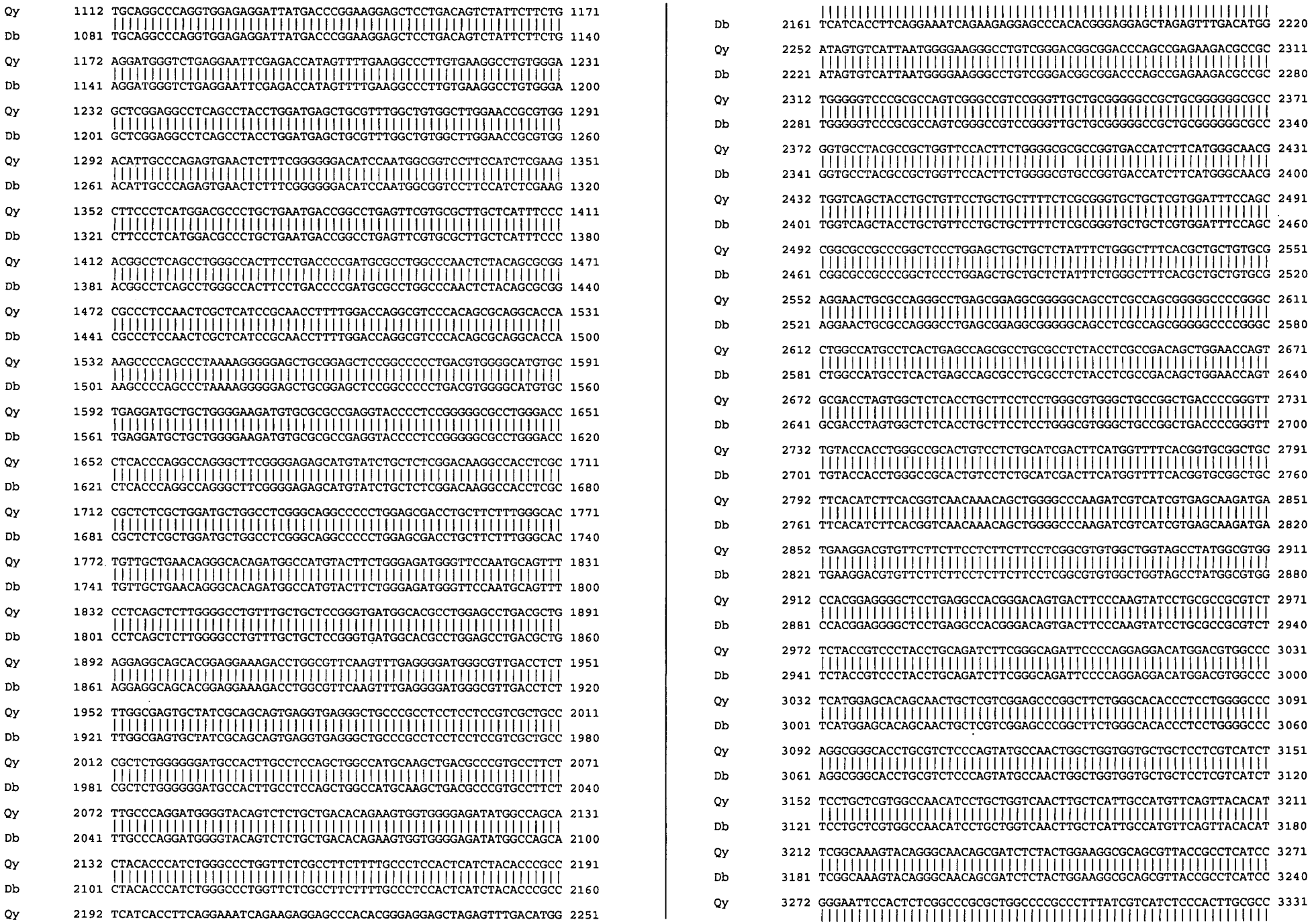
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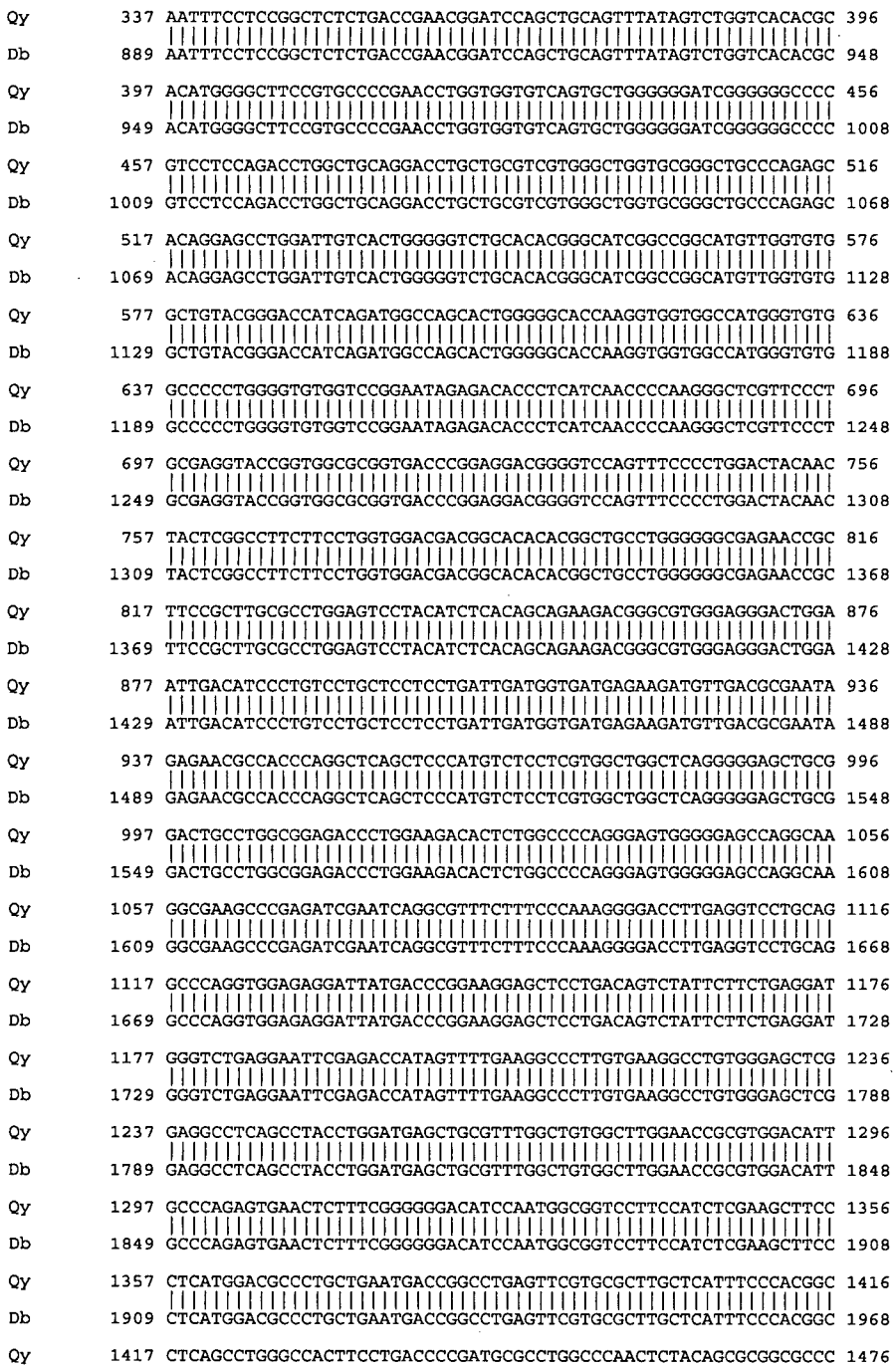
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RESULT 6
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AC   ADN39239;
XX
DT   17-JUN-2004  (first entry)
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DE   Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:557.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine; gene; ss.
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XX
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XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036810.
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PR   13-NOV-2001; 2001US-0350666P.
PR   21-NOV-2001; 2001US-0332464P.
PR   29-NOV-2001; 2001US-0334393P.
PR   03-DEC-2001; 2001US-0335394P.
PR   14-DEC-2001; 2001US-0340376P.
PR   08-JAN-2002; 2002US-0347211P.
PR   10-JAN-2002; 2002US-0347349P.
PR   08-FEB-2002; 2002US-0355250P.
PR   13-FEB-2002; 2002US-0356714P.
PR   20-FEB-2002; 2002US-0359077P.
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PR   12-APR-2002; 2002US-0372246P.
PR   05-JUN-2002; 2002US-0386614P.
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PR   09-SEP-2002; 2002US-0409450P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D,  Aziz N,  Ginsburg WM,  Gish KC,  Glynne R,  Hevezi PA;
PI   Mack DH,  Murray R,  Watson SR,  Wilson KE,  Zlotnik A;
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DR   WPI; 2003-468649/44.
DR   P-PSDB; ADN39240.
XX
PT   Determining the presence or absence of a pathological cell in a patient,
PT   useful for diagnosing, prognosing or treating cancer, comprises detecting
PT   a nucleic acid in a biological sample.
XX
PS   Claim 8; SEQ ID NO 557; 1385pp; English.
XX
CC   The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC   whose expression is upregulated or downregulated in specific cancers or
CC   other diseases such as angiogenic or fibrotic disorders, and to methods
CC   of determining the presence or absence of a pathological cell in a
CC   patient by detecting a nucleic acid at least 80% identical to those of
CC   the invention or by detecting a polypeptide of the invention. The
CC   invention also relates to expression vectors and host cells comprising a
CC   nucleic acid of the invention; antibodies which specifically bind a
CC   polypeptide of the invention; use of such antibodies for drug targeting;
CC   and methods of screening for modulators of activity or expression of the
CC   polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC   antibodies and methods are useful for diagnosing, prognosing and treating
CC   cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC   atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC   neovascularistaion syndromes, scarring and uterine fibroids. They may
CC   also be useful in wound healing and in contraception. The present
CC   sequence represents a nucleic acid sequence of the invention.
XX
SQ   Sequence 4641 BP; 808 A; 1459 C; 1432 G; 942 T; 0 U; 0 Other;

  Query Match           94.7%;  Score 3845;  DB 11;  Length 4641;
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Db 1429 ATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGCGAATA 1488
Qy 937 GAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAGCTGCG 996
Db 1489 GAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAGCTGCG 1548
Qy 997 GACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCAGGCAA 1056
Db 1549 GACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCAGGCAA 1608
Qy 1057 GGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCCTGCAG 1116
Db 1609 GGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCCTGCAG 1668
Qy 1117 GCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTGAGGAT 1176
Db 1669 GCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTGAGGAT 1728
Qy 1177 GGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGAGCTCG 1236
Db 1729 GGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGAGCTCG 1788
Qy 1237 GAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGGACATT 1296
Db 1789 GAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGGACATT 1848
Qy 1297 GCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAGCTTCC 1356
Db 1849 GCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAGCTTCC 1908
Qy 1357 CTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGC 1416
Db 1909 CTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGC 1968
Qy 1417 CTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCC 1476
Db 1969 CTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCC 2028
Qy 1477 TCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCC 1536
Db 2029 TCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCC 2088
Qy 1537 CCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGG 1596
Db 2089 CCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGG 2148
Qy 1597 ATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCAC 1656
Db 2149 ATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCAC 2208
Qy 1657 CCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTC 1716
Db 2209 CCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTC 2268
Qy 1717 TCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTG 1776
Db 2269 TCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTG 2328
Qy 1777 CTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCA 1836
Db 2329 CTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCA 2388
Qy 1837 GCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAG 1896
Db 2389 GCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAG 2448
Qy 1897 GCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGC 1956
Db 2449 GCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGC 2508
Qy 1957 GAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTC 2016
Db 2509 GAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTC 2568
Qy 2017 TGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCC 2076
Db 2569 TGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCC 2628
Qy 2077 CAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACA 2136
Db 2629 CAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACA 2688
Qy 2137 CCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATC 2196
Db 2689 CCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATC 2748
Qy 2197 ACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGT 2256
Db 2749 ACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGT 2808
Qy 2257 GTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGG 2316
Db 2809 GTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGG 2868
Qy 2317 GTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGC 2376
Db 2869 GTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGC 2928
Qy 2377 CTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTC 2436
Db 2929 CTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTC 2988
Qy 2437 AGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCG 2496
Db 2989 AGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCG 3048
Qy 2497 CCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAA 2556

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Qy       2557 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2616
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3109 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 3168

Qy       2617 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2676
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3169 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 3228

Qy       2677 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2736
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3229 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 3288

Qy       2737 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2796
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3289 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 3348

Qy       2797 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2856
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3349 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 3408

Qy       2857 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2916
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3409 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 3468

Qy       2917 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2976
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3469 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 3528

Qy       2977 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 3036
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3529 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 3588

Qy       3037 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3096
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3589 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3648

Qy       3097 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3156
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3649 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3708

Qy       3157 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3216
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3709 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3768

Qy       3217 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3276
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3769 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3828

Qy       3277 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3336
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3829 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3888

Qy       3337 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3396
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3889 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3948

Qy       3397 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3456
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3949 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 4008

Qy       3457 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3516
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Db       4009 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 4068

Qy       3517 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4069 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 4128

Qy       3577 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3636
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4129 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 4188

Qy       3637 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3696
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4189 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 4248

Qy       3697 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 3756
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4249 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 4308

Qy       3757 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 3816
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4309 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 4368

Qy       3817 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 3876
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4369 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 4428

Qy       3877 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 3936
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4429 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 4488

Qy       3937 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 3996
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4489 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 4548

Qy       3997 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 4056
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4549 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 4608

Qy       4057 AAAAA 4061
             |||||
Db       4609 AAAAA 4613
```

RESULT 7
ADL06463
ID ADL06463 standard; cDNA; 3898 BP.
XX
AC ADL06463;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #43.
XX
KW Human; tumour-associated antigenic target; TAT; cell death; tumour;
KW cancer; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004016225-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US025892.
XX
PR 19-AUG-2002; 2002US-0404809P.
PR 21-AUG-2002; 2002US-0405645P.
PR 23-SEP-2002; 2002US-0413192P.
PR 15-OCT-2002; 2002US-0419008P.
PR 15-NOV-2002; 2002US-0426847P.
PR 02-JUL-2003; 2003US-0484959P.
XX
PA (GETH) GENENTECH INC.
XX
PI Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;
PI Spencer SD, Wu TD, Zhang Z;
XX
DR WPI; 2004-257144/24.
DR P-PSDB; ADL06543.
XX
PT New antibody that binds to a tumor-associated antigenic target (TAT)
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating cancer.

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XX
PS   Claim 1; SEQ ID NO 43; 319pp; English.
XX
CC   The present invention relates to the isolation of human tumour-associated
CC   antigenic target (TAT) polynucleotide and polypeptide sequences. Also
CC   disclosed is an antibody that binds to a TAT polypeptide. The antibody is
CC   a monoclonal antibody, an antibody fragment, a chimeric antibody or a
CC   humanised antibody. It is conjugated to a growth inhibitory agent. It is
CC   produced in bacteria or in CHO cells and induces death of a cell to which
CC   it binds. The antibody is useful for preparing a composition for
CC   diagnosing or treating tumours and cancer. The present sequence
CC   represents a human TAT cDNA sequence of the invention.
XX
SQ   Sequence 3898 BP; 685 A; 1207 C; 1235 G; 771 T; 0 U; 0 Other;

  Query Match             93.9%;  Score 3812.2;  DB 12;  Length 3898;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 3848;  Conservative    0;  Mismatches   23;  Indels    2;  Gaps    2;

Qy        190 CCCCGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCCGTGGTGACC 249
              |||| |  |||||||||||||||||||||||| || ||||||||||||||||||||||||
Db          7 CCCCCGGACGCCCACCCCGCAGTGGCCATGGA-GAAGCCTTCGGGGCAGCCGTGGTGACC 65

Qy        250 GTGTGGGACAGCGATGCAC-ACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGA 308
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db         66 GTGTGGGACAGCGATGCACAACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGA 125

Qy        309 CTTCACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCC 368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CTTCACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCC 185

Qy        369 AGCTGCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGT 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AGCTGCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGT 245

Qy        429 GTCAGTGCTGGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCG 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GTCAGTGCTGGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCG 305

Qy        489 TCGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCA 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TCGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCA 365

Qy        549 CACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGG 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGG 425

Qy        609 GGGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACAC 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GGGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACAC 485

Qy        669 CCTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGA 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CCTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGA 545

Qy        729 CGGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCAC 788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CGGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCAC 605

Qy        789 ACACGGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACA 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 ACACGGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACA 665

Qy        849 GCAGAAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGA 908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 GCAGAAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGA 725

Qy        909 TGGTGATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCT 968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TGGTGATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCT 785

Qy        969 CCTCGTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCT 1028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        786 CCTCGTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCT 845

Qy       1029 GGCCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTT 1088
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         846 GGCCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTT 905

Qy       1089 TCCCAAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGA 1148
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Db         906 TCCCAAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGA 965

Qy       1149 GCTCCTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAA 1208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         966 GCTCCTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAA 1025

Qy       1209 GGCCCTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTT 1268
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Db        1026 GGCCCTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTT 1085

Qy       1269 GGCTGTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCA 1328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1086 GGCTGTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCA 1145

Qy       1329 ATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGA 1388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1146 ATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGA 1205

Qy       1389 GTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCG 1448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1206 GTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCG 1265

Qy       1449 CCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCA 1508
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Qy       1509 GGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCG 1568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1326 GGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCG 1385

Qy       1569 GCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTA 1628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1386 GCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTA 1445

Qy       1629 CCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCT 1688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1446 CCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCT 1505

Qy       1689 GCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTG 1748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1506 GCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTG 1565

Qy       1749 GAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTG 1808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1809 GGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGAT 1868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1626 GGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGAT 1685

Qy       1869 GGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTT 1928
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1686 GGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTT 1745

Qy       1929 TGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGC 1988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1746 TGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGC 1805

Qy       1989 CCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCAT 2048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1806 CCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCAT 1865

Qy       2049 GCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAA 2108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1866 GCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAA 1925
```

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Qy       2109 GTGGTGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTG 2168
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Db       1926 GTGGTGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTG 1985

Qy       2169 CCCTCCACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACG 2228
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Db       1986 CCCTCCACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACG 2045

Qy       2229 GGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGC 2288
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2046 GGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGC 2105

Qy       2289 GGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTG 2348
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2106 GGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTG 2165

Qy       2349 CGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCC 2408
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2166 CGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCC 2225

Qy       2409 GGTGACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCG 2468
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Db       2226 GGTGACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCTTGCTGCTTTTCTCGCG 2285

Qy       2469 GGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTT 2528
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Db       2286 GGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTT 2345

Qy       2529 CTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAG 2588
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Db       2346 CTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAG 2405

Qy       2589 CCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTA 2648
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Db       2406 CCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTA 2465

Qy       2649 CCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGT 2708
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2466 CCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGT 2525

Qy       2709 GGGCTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTT 2768
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Qy       2769 CATGGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAA 2828
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Qy       2829 GATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGT 2888
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Db       2646 GATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGT 2705

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Qy       3009 CCAGGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTT 3068
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Qy       3129 GGTGGTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCT 3188
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Qy       3189 CATTGCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAA 3248
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Db       3006 CATTGCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAA 3065

Qy       3249 GGCGCAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTT 3308
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Db       3066 GGCGCAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTT 3125

Qy       3309 TATCGTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCC 3368
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Db       3306 CAAGCGGGAGAGCGACTCCGAGCGTCTGGAGCGCACGTCCCAGAAGGTGGACTTGGCACT 3365

Qy       3549 GAAACAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGT 3608
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Qy       3609 CCAGCAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCT 3668
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Qy       3669 GCCCCCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGC 3728
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Qy       3729 GGACTTCAAGGAGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCC 3788
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Qy       3789 TCGGCCCCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACT 3848
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Db       3606 TCGGCCCCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACT 3665

Qy       3849 GTCAGGACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAG 3908
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Db       3666 GTCAGGACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAG 3725

Qy       3909 AACCAGTCCCAGCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGC 3968
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Qy       3969 TGCAGGGTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATTCCTCACAC 4028
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Qy       4029 TGGGGAAATAAAGCCATTTCAGAGGAAAAAAAA 4061
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Db       3846 TGGGGAAATAAAGCCATTTCAGAGGAAAAAAAA 3878
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RESULT 8
ABK92167
ID   ABK92167 standard; DNA; 3810 BP.
XX
AC   ABK92167;
XX
DT   15-AUG-2002  (first entry)
XX
DE   Prostate cancer-associated DNA sequence #53.
XX
KW   Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW   gene therapy; gene; ds.
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XX
OS Mammalia.
XX
PN WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032045.
XX
PR 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-0263957P.
PR 16-MAR-2001; 2001US-0276791P.
PR 16-MAR-2001; 2001US-0276888P.
PR 06-APR-2001; 2001US-0281922P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0288589P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
DR WPI; 2002-471335/50.
DR P-PSDB; ABG61852.
XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
XX
PS Claim 22; Page 339-340; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridise to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX
SQ Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;

Query Match 92.6%; Score 3759.6; DB 6; Length 3810;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3771; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy        272 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 331
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Db          1 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 60

Qy        332 ACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCA 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        392 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 451
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Db        121 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 180

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Qy        692 TCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACT 751
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Qy        812 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 871
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Db        541 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 600

Qy        872 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 931
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Db        601 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 660

Qy        932 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 991
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Qy        992 CTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCA 1051
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Qy       1052 GGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCC 1111
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Qy       1112 TGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTG 1171
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Db        841 TGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTG 900

Qy       1172 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGA 1231
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Qy       1232 GCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGG 1291
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Qy       1292 ACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAG 1351
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Qy       1352 CTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCC 1411
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Qy       1532 AAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGC 1591
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Qy       1592 TGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACC 1651
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Db      1321 TGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACC 1380
Qy      1652 CTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGC 1711
Db      1381 CTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGC 1440
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Db      1561 CCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTG 1620
Qy      1892 AGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCT 1951
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Qy      1952 TTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCC 2011
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Qy      2012 CGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCT 2071
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Qy      2252 ATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGC 2311
Db      1981 ATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGC 2040
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Db      2041 TGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCC 2100
Qy      2372 GGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACG 2431
Db      2101 GGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACG 2160
Qy      2432 TGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGC 2491
Db      2161 TGGTCAGCTACCTGCTGTTCTTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGC 2220
Qy      2492 CGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCG 2551
Db      2221 CGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCG 2280
Qy      2552 AGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGC 2611
Db      2281 AGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGC 2340
Qy      2612 CTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGT 2671
Db      2341 CTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGT 2400
Qy      2672 GCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTT 2731
Db      2401 GCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTT 2460
Qy      2732 TGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGC 2791
Db      2461 TGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGC 2520
Qy      2792 TTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGA 2851
Db      2521 TTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGA 2580
Qy      2852 TGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGG 2911
Db      2581 TGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGG 2640
Qy      2912 CCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCT 2971
Db      2641 CCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCT 2700
Qy      2972 TCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCC 3031
Db      2701 TCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCC 2760
Qy      3032 TCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCC 3091
Db      2761 TCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCC 2820
Qy      3092 AGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCT 3151
Db      2821 AGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCT 2880
Qy      3152 TCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACAT 3211
Db      2881 TCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACAT 2940
Qy      3212 TCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCC 3271
Db      2941 TCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCC 3000
Qy      3272 GGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCC 3331
Db      3001 GGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCC 3060
Qy      3332 TCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCG 3391
Db      3061 TCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCG 3120
Qy      3392 AGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGG 3451
Db      3121 AGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGG 3180
Qy      3452 TGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGC 3511
Db      3181 TGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGC 3240
Qy      3512 GTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCG 3571
Db      3241 GTCTGGAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCG 3300
Qy      3572 AGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGG 3631
Db      3301 AGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGG 3360
Qy      3632 GGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCC 3691
Db      3361 GGTGGGTGACGTAGGCCGTTAGCAGCTCTGCCATGTTGCCCTCAGGTGGGCCGCCACCCC 3420
Qy      3692 CTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCAC 3751
Db      3421 TTGACCTGCATGGGTCCAAAGAGTGAGCCATGCTGGCGGATTTTAAGGAGAAGCCCCCAC 3480
Qy      3752 AGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCT 3811
Db      3481 AGGGGATTTTGCTCTTAGAGTAAGGCTCATGTGGGCCTCGGCCCCCGCACCTGGTGGCCT 3540
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Qy       3812 TGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGT 3871
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGT 3600

Qy       3872 CATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGAT 3931
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGAT 3660

Qy       3932 CAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGG 3991
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGG 3720

Qy       3992 GACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 4051
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 3780

Qy       4052 GGAAAAAAAA 4061
             ||||||||||
Db       3781 GGAAAAAAAA 3790
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RESULT 9
ADR66772
ID ADR66772 standard; DNA; 3810 BP.
XX
AC ADR66772;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived DNA SEQ ID 65 #4.
XX
KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis; ds.
XX
OS Homo sapiens.
XX
PN WO2004076614-A2.
XX
PD 10-SEP-2004.
XX
PF 22-FEB-2004; 2004WO-DE000433.
XX
PR 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemmendorf T, Kinnemann H, Roepcke S;
PI Xinzhong L, Staub E;
XX
DR WPI; 2004-653386/63.
XX
PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
PS Claim 1; Page 1439; 1607pp; German.
XX
CC This invention describes novel cytostatic polynucleotide and polypeptide
CC sequences which can be used in a method for diagnosing prostatic cancer
CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotype, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated
CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.
XX
SQ Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;

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  Query Match             92.6%;  Score 3759.6;  DB 13;  Length 3810;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 3771;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy        272 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 60

Qy        332 ACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCA 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCA 120

Qy        392 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 180

Qy        452 GCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCC 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCC 240

Qy        512 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 300

Qy        572 GTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGG 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGG 360

Qy        632 GTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGT 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGT 420

Qy        692 TCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACT 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACT 480

Qy        752 ACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGA 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGA 540

Qy        812 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 871
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 600

Qy        872 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 660

Qy        932 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 991
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Db        661 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 720
Qy        992 CTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCA 1051
Db        721 CTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCA 780
Qy       1052 GGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCC 1111
Db        781 GGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCC 840
Qy       1112 TGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTG 1171
Db        841 TGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTG 900
Qy       1172 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGA 1231
Db        901 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGA 960
Qy       1232 GCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGG 1291
Db        961 GCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGG 1020
Qy       1292 ACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAG 1351
Db       1021 ACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAG 1080
Qy       1352 CTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCC 1411
Db       1081 CTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCC 1140
Qy       1412 ACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGG 1471
Db       1141 ACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGG 1200
Qy       1472 CGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCA 1531
Db       1201 CGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCA 1260
Qy       1532 AAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGC 1591
Db       1261 AAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGC 1320
Qy       1592 TGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGGCGCCTGGGACC 1651
Db       1321 TGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGGCGCCTGGGACC 1380
Qy       1652 CTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGC 1711
Db       1381 CTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGC 1440
Qy       1712 CGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCAC 1771
Db       1441 CGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCAC 1500
Qy       1772 TGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTT 1831
Db       1501 TGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTT 1560
Qy       1832 CCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTG 1891
Db       1561 CCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTG 1620
Qy       1892 AGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCT 1951
Db       1621 AGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCT 1680
Qy       1952 TTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCC 2011
Db       1681 TTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCC 1740
Qy       2012 CGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCT 2071
Db       1741 CGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCT 1800
Qy       2072 TTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCA 2131
Db       1801 TTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCA 1860
Qy       2132 CTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCC 2191
Db       1861 CTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCC 1920
Qy       2192 TCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGG 2251
Db       1921 TCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGG 1980
Qy       2252 ATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGC 2311
Db       1981 ATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGC 2040
Qy       2312 TGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCC 2371
Db       2041 TGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCC 2100
Qy       2372 GGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACG 2431
Db       2101 GGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACG 2160
Qy       2432 TGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGC 2491
Db       2161 TGGTCAGCTACCTGCTGTTCTTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGC 2220
Qy       2492 CGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCG 2551
Db       2221 CGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCG 2280
Qy       2552 AGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGC 2611
Db       2281 AGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGC 2340
Qy       2612 CTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGT 2671
Db       2341 CTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGT 2400
Qy       2672 GCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTT 2731
Db       2401 GCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTT 2460
Qy       2732 TGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGC 2791
Db       2461 TGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGC 2520
Qy       2792 TTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGA 2851
Db       2521 TTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGA 2580
Qy       2852 TGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGG 2911
Db       2581 TGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGG 2640
Qy       2912 CCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCT 2971
Db       2641 CCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCT 2700
Qy       2972 TCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCC 3031
Db       2701 TCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCC 2760
Qy       3032 TCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCC 3091
Db       2761 TCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCC 2820
Qy       3092 AGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCT 3151
Db       2821 AGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCT 2880
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Qy       3152 TCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACAT 3211
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 TCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACAT 2940

Qy       3212 TCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCC 3271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 TCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCC 3000

Qy       3272 GGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCC 3331
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 GGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCC 3060

Qy       3332 TCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCG 3391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCG 3120

Qy       3392 AGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGG 3451
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 AGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGG 3180

Qy       3452 TGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGC 3511
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 TGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGC 3240

Qy       3512 GTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCG 3571
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GTCTGGAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCG 3300

Qy       3572 AGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGG 3631
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 AGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGG 3360

Qy       3632 GGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCC 3691
             |||||||| |  ||||| | ||| |||||||| || ||||| ||||||||||||||||||
Db       3361 GGTGGGTGACGTAGGCCGTTAGCAGCTCTGCCATGTTGCCCTCAGGTGGGCCGCCACCCC 3420

Qy       3692 CTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCAC 3751
               |||||||| |||||||||||| |||||| |||||||||| || |||||||||||||||||
Db       3421 TTGACCTGCATGGGTCCAAAGAGTGAGCCATGCTGGCGGATTTTAAGGAGAAGCCCCCAC 3480

Qy       3752 AGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCT 3811
             |||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||
Db       3481 AGGGGATTTTGCTCTTAGAGTAAGGCTCATGTGGGCCTCGGCCCCCGCACCTGGTGGCCT 3540

Qy       3812 TGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGT 3871
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGT 3600

Qy       3872 CATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGAT 3931
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGAT 3660

Qy       3932 CAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGG 3991
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGG 3720

Qy       3992 GACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 4051
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 3780

Qy       4052 GGAAAAAAAA 4061
             ||||||||||
Db       3781 GGAAAAAAAA 3790


RESULT 10
ADR65869
ID   ADR65869 standard; DNA; 3810 BP.
XX
AC   ADR65869;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human prostatic carcinoma derived DNA SEQ ID 65 #1.
XX
KW   human; cytostatic; diagnosis; prostatic cancer;
KW   differential expression analysis; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004076614-A2.
XX
PD   10-SEP-2004.
XX
PF   22-FEB-2004; 2004WO-DE000433.
XX
PR   27-FEB-2003; 2003DE-01009985.
PR   14-MAY-2003; 2003DE-01022134.
XX
PA   (HINZ/) HINZMANN B.
PA   (DAHL/) DAHL E.
PA   (ROSE/) ROSENTHAL A.
PA   (HERM/) HERMANN K.
PA   (PILA/) PILARSKY C.
XX
PI   Hinzmann B,  Dahl E,  Rosenthal A,  Hermann K,  Pilarsky C,  Specht T;
PI   Schmitt A,  Beckmann G,  Bruemmendorf T,  Kinnemann H,  Roepcke S;
PI   Xinzhong L,  Staub E;
XX
DR   WPI; 2004-653386/63.
XX
PT   New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT   useful for diagnosis, treatment and in screening for specific binding
PT   agents.
XX
PS   Claim 1; Page 269; 1607pp; German.
XX
CC   This invention describes novel cytostatic polynucleotide and polypeptide
CC   sequences which can be used in a method for diagnosing prostatic cancer
CC   or the risk of developing prostatic cancer. Diagnosis is based on
CC   determining over transcription or over expression of the sequences in
CC   prostatic tissue. Screening for inhibitors of the sequences or detection
CC   substances involves a binding assay, any compounds that bind are
CC   selected, optionally after deconvolution of mixtures. Detection of a
CC   predetermined minimum level of the reporter indicates the presence of
CC   tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC   short-interfering RNA or ribozymes; an organic molecule of molecular
CC   weight below 5000, preferably 300, that binds to the polypeptide; an
CC   aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC   polypeptide, preferably humanised or human; an anti-idiotype, non-human
CC   (monoclonal) antibody directed against Ab or any of the above derivatised
CC   with a reporter group, cell toxin, immunostimulatory molecules and/or
CC   radioisotope. The polynucleotides are identified in human prostatic
CC   cancer by differential expression analysis, using DNA microarrays,
CC   between normal and tumorous tissues, with (over)expression being detected
CC   by quantitative PCR. Analysis of prostatic cancer samples showed that
CC   CD24 was upregulated in many of them. Sections of tissue, isolated from
CC   prostatic cancer patients, or subjects at risk, were incubated
CC   sequentially with anti-human CD4 murine monoclonal antibodies;
CC   biotinylated second antibody; streptavidin-conjugated horseradish
CC   peroxidase and then diaminobenzidine as colour former (brown). The
CC   samples were counterstained with hemalum (blue). Malignant cells stained
CC   strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC   adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC   lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC   polynucleotide and polypeptide sequences used in the method of the
CC   invention.
XX
SQ   Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;

  Query Match             92.6%;  Score 3759.6;  DB 13;  Length 3810;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 3771;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy        272 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 331
```

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Db        1 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 60
Qy      332 ACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCA 391
Db       61 ACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCA 120
Qy      392 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 451
Db      121 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 180
Qy      452 GCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCC 511
Db      181 GCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCC 240
Qy      512 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 571
Db      241 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 300
Qy      572 GTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGG 631
Db      301 GTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGG 360
Qy      632 GTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGT 691
Db      361 GTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGT 420
Qy      692 TCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACT 751
Db      421 TCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACT 480
Qy      752 ACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGA 811
Db      481 ACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGA 540
Qy      812 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 871
Db      541 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 600
Qy      872 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 931
Db      601 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 660
Qy      932 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 991
Db      661 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 720
Qy      992 CTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCA 1051
Db      721 CTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCA 780
Qy     1052 GGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCC 1111
Db      781 GGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCC 840
Qy     1112 TGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTG 1171
Db      841 TGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTG 900
Qy     1172 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGA 1231
Db      901 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGA 960
Qy     1232 GCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGG 1291
Db      961 GCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGG 1020
Qy     1292 ACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAG 1351
Db     1021 ACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAG 1080
Qy     1352 CTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCC 1411
Db     1081 CTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCC 1140
Qy     1412 ACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGG 1471
Db     1141 ACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGG 1200
Qy     1472 CGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCA 1531
Db     1201 CGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCA 1260
Qy     1532 AAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGC 1591
Db     1261 AAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGC 1320
Qy     1592 TGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACC 1651
Db     1321 TGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACC 1380
Qy     1652 CTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGC 1711
Db     1381 CTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGC 1440
Qy     1712 CGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCAC 1771
Db     1441 CGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCAC 1500
Qy     1772 TGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTT 1831
Db     1501 TGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTT 1560
Qy     1832 CCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTG 1891
Db     1561 CCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTG 1620
Qy     1892 AGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCT 1951
Db     1621 AGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCT 1680
Qy     1952 TTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCC 2011
Db     1681 TTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCC 1740
Qy     2012 CGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCT 2071
Db     1741 CGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCT 1800
Qy     2072 TTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCA 2131
Db     1801 TTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCA 1860
Qy     2132 CTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCC 2191
Db     1861 CTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCC 1920
Qy     2192 TCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGG 2251
Db     1921 TCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGG 1980
Qy     2252 ATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGC 2311
Db     1981 ATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGC 2040
Qy     2312 TGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCC 2371
Db     2041 TGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCC 2100
Qy     2372 GGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACG 2431
Db     2101 GGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACG 2160
Qy     2432 TGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGC 2491
Db     2161 TGGTCAGCTACCTGCTGTTCTTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGC 2220
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Qy       2492 CGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCG 2551
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCG 2280

Qy       2552 AGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGC 2611
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 AGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGC 2340

Qy       2612 CTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGT 2671
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 CTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGT 2400

Qy       2672 GCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTT 2731
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTT 2460

Qy       2732 TGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGC 2791
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 TGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGC 2520

Qy       2792 TTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGA 2851
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGA 2580

Qy       2852 TGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGG 2911
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 TGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGG 2640

Qy       2912 CCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCT 2971
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCT 2700

Qy       2972 TCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCC 3031
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 TCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCC 2760

Qy       3032 TCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCC 3091
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCC 2820

Qy       3092 AGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCT 3151
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 AGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCT 2880

Qy       3152 TCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACAT 3211
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 TCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACAT 2940

Qy       3212 TCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCC 3271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 TCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCC 3000

Qy       3272 GGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCC 3331
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 GGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCC 3060

Qy       3332 TCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCG 3391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCG 3120

Qy       3392 AGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGG 3451
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 AGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGG 3180

Qy       3452 TGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGC 3511
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 TGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGC 3240

Qy       3512 GTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCG 3571
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GTCTGGAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCG 3300

Qy       3572 AGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGG 3631
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 AGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGG 3360

Qy       3632 GGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCC 3691
             |||||||| | ||||| | ||| |||||||| || ||||| ||||||||||||||||||||
Db       3361 GGTGGGTGACGTAGGCCGTTAGCAGCTCTGCCATGTTGCCCTCAGGTGGGCCGCCACCCC 3420

Qy       3692 CTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCAC 3751
              |||||||| |||||||||||| |||||| |||||||||| || ||||||||||||||||
Db       3421 TTGACCTGCATGGGTCCAAAGAGTGAGCCATGCTGGCGGATTTTAAGGAGAAGCCCCCAC 3480

Qy       3752 AGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCT 3811
             ||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||||||
Db       3481 AGGGGATTTTGCTCTTAGAGTAAGGCTCATGTGGGCCTCGGCCCCCGCACCTGGTGGCCT 3540

Qy       3812 TGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGT 3871
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGT 3600

Qy       3872 CATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGAT 3931
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGAT 3660

Qy       3932 CAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGG 3991
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGG 3720

Qy       3992 GACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 4051
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 3780

Qy       4052 GGAAAAAAAA 4061
              ||||||||||
Db       3781 GGAAAAAAAA 3790
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RESULT 11
ADS12778
ID   ADS12778 standard; cDNA; 3810 BP.
XX
AC   ADS12778;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Human TRPM4a splicing variant cDNA sequence.
XX
KW   transient receptor potential cation channel; subfamily M; member 4;
KW   TRPM4; phospholipase A1-A; PLA1A; butyryl coenzyme A synthetase 1; BUCS1;
KW   prostate cancer; TRPM4a; gene; ss; splicing variant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             324. .3374
FT                   /*tag=  a
FT                   /product= "Human TRPM4a splicing variant protein"
XX
PN   JP2004267118-A.
XX
PD   30-SEP-2004.
XX
PF   10-MAR-2003; 2003JP-00063578.
XX
PR   10-MAR-2003; 2003JP-00063578.
XX
PA   (SANY ) SANKYO CO LTD.
XX
DR   WPI; 2004-693915/68.
DR   P-PSDB; ADS12779.
XX
PT   Detecting prostatic cancer, comprises extracting RNA fractions from test
PT   substance of subject and normal human, measuring and analyzing the
```

PT difference in e.g., phospholipase A1-A and butyryl coenzyme A synthetase
PT expression levels.
XX
PS Claim 1; SEQ ID NO 5; 126pp; Japanese.
XX
CC The invention comprises a method for detecting prostatic cancer in a
CC subject. The method involves measuring the expression levels of specific
CC genes: transient receptor potential cation channel, subfamily M, member 4
CC (TRPM4); phospholipase A1-A (PLA1A); and butyryl coenzyme A synthetase 1
CC (BUCS1). The method of the invention is useful for the detection and
CC treatment of prostate cancer. The present cDNA sequence encodes the human
CC TRPM4a splicing variant protein of the invention.
XX
SQ Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;

Query Match 92.6%; Score 3759.6; DB 13; Length 3810;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3771; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy       272 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 331
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 60

Qy       332 ACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCA 391
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 ACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCA 120

Qy       392 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 451
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 180

Qy       452 GCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCC 511
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCC 240

Qy       512 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 571
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 300

Qy       572 GTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGG 631
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Qy       632 GTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGT 691
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Db       361 GTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGT 420

Qy       692 TCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACT 751
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Db       421 TCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACT 480

Qy       752 ACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGA 811
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Db       481 ACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGA 540

Qy       812 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 871
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Db       541 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 600

Qy       872 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 931
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 660

Qy       932 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 991
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 720

Qy       992 CTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCA 1051
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 CTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCA 780

Qy      1052 GGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCC 1111
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 GGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCC 840

Qy      1112 TGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTG 1171
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 TGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTG 900

Qy      1172 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGA 1231
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      1232 GCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGG 1291
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGG 1020

Qy      1292 ACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAG 1351
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAG 1080

Qy      1352 CTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCC 1411
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCC 1140

Qy      1412 ACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGG 1471
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 ACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGG 1200

Qy      1472 CGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCA 1531
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 CGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCA 1260

Qy      1532 AAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGC 1591
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 AAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGC 1320

Qy      1592 TGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACC 1651
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 TGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACC 1380

Qy      1652 CTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGC 1711
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 CTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGC 1440

Qy      1712 CGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCAC 1771
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      1772 TGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTT 1831
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Db      1501 TGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTT 1560

Qy      1832 CCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTG 1891
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Db      1561 CCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTG 1620

Qy      1892 AGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCT 1951
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Db      1621 AGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCT 1680

Qy      1952 TTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCC 2011
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Db      1681 TTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCC 1740

Qy      2012 CGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCT 2071
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCT 1800

Qy      2072 TTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCA 2131
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Db      1801 TTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCA 1860

Qy      2132 CTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCC 2191
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 CTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCC 1920
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Qy      2192 TCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGG 2251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 TCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGG 1980

Qy      2252 ATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGC 2311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 ATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGC 2040

Qy      2312 TGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCC 2371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 TGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCC 2100

Qy      2372 GGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACG 2431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 GGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACG 2160

Qy      2432 TGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGC 2491
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      2161 TGGTCAGCTACCTGCTGTTCTTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGC 2220

Qy      2492 CGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCG 2551
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Db      2221 CGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCG 2280

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Db      2341 CTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGT 2400

Qy      2672 GCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTT 2731
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Db      2401 GCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTT 2460

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Db      2461 TGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGC 2520

Qy      2792 TTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGA 2851
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Qy      2852 TGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGG 2911
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Db      2581 TGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGG 2640

Qy      2912 CCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCT 2971
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Db      2641 CCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCT 2700

Qy      2972 TCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCC 3031
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Qy      3032 TCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCC 3091
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Db      2761 TCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCC 2820

Qy      3092 AGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCT 3151
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Db      2821 AGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCT 2880

Qy      3152 TCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACAT 3211
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Db      2941 TCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCC 3000

Qy      3272 GGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCC 3331
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Db      3001 GGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCC 3060

Qy      3332 TCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCG 3391
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Qy      3392 AGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGG 3451
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Qy      3452 TGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGC 3511
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Qy      3512 GTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCG 3571
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Db      3241 GTCTGGAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCG 3300

Qy      3572 AGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGG 3631
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Db      3301 AGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGG 3360

Qy      3632 GGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCC 3691
             |||||||| | ||||| | ||| |||||||| || ||||| ||||||||||||||||||
Db      3361 GGTGGGTGACGTAGGCCGTTAGCAGCTCTGCCATGTTGCCCTCAGGTGGGCCGCCACCCC 3420

Qy      3692 CTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCAC 3751
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Qy      3752 AGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCT 3811
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Db      3481 AGGGGATTTTGCTCTTAGAGTAAGGCTCATGTGGGCCTCGGCCCCCGCACCTGGTGGCCT 3540

Qy      3812 TGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGT 3871
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Db      3541 TGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGT 3600

Qy      3872 CATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGAT 3931
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Qy      3932 CAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGG 3991
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Db      3661 CAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGG 3720

Qy      3992 GACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 4051
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3721 GACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGA 3780

Qy      4052 GGAAAAAAAA 4061
             ||||||||||
Db      3781 GGAAAAAAAA 3790
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RESULT 12
AAH76383
ID AAH76383 standard; cDNA; 3900 BP.
XX
AC AAH76383;
XX
DT 30-NOV-2001 (first entry)
XX
DE Human TLCC polypeptide encoding cDNA.
XX
KW TLCC; transient receptor potential; TRP; TRP-like calcium channel; human;
KW hepatotropic; cardiant; antiarteriosclerotic; antiinflammatory; virucide;
KW cytostatic; analgesic; cerebroprotective; nootropic; neuroprotective;
KW gene therapy; ss.
XX
OS Homo sapiens.

```
XX
FH   Key             Location/Qualifiers
FT   CDS             138. .3527
FT                   /*tag=  a
FT                   /product= "TLCC polypeptide"
FT                   /note= "coding sequence (AAH76384) specifically claimed"
XX
PN   WO200162794-A2.
XX
PD   30-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US005529.
XX
PR   22-FEB-2000; 2000US-00510706.
PR   31-MAY-2000; 2000US-00583373.
PR   08-AUG-2000; 2000US-00634669.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Glucksmann MA,  Curtis RAJ,  Lora JM;
XX
DR   WPI; 2001-557700/62.
DR   P-PSDB; AAB85974.
XX
PT   New isolated nucleic acid encoding a transient receptor potential-like
PT   calcium channel for identifying modulators that can be used to treat
PT   hepatic or cardiovascular disorders.
XX
PS   Claim 1; Fig 1A-D; 160pp; English.
XX
CC   The invention provides isolated nucleic acids encoding a human transient
CC   receptor potential (TRP) family member, called TRP-like calcium channel
CC   (TLCC) polypeptide. The TLCC polypeptide can be expressed by standard
CC   recombinant methodology. The TLCC polynucleotides and polypeptide are
CC   used to identify modulators that can be used to treat a hepatic or a
CC   cardiovascular disorder, such as liver fibrosis or atherosclerosis. Other
CC   disorders that can be treated are hepatitis, liver tumours, cirrhosis of
CC   the liver, hemochromatosis, liver parasite induced disorders, central
CC   nervous system disorders, pain disorders, or disorders of cellular
CC   growth, differentiation or migration. The TLCC polynucleotides,
CC   polypeptide, protein homologs and antibodies to the proteins can be used
CC   in predictive medicine (e.g. diagnostic assays, prognostic assays,
CC   monitoring clinical trials and pharmacogenetics). Anti-TLCC antibodies
CC   can isolate TLCC proteins, regulate the bioavailablility of TLCC
CC   proteins, and modulate TLCC activity. The present sequence represents a
CC   cDNA encoding the human TLCC polypeptide
XX
SQ   Sequence 3900 BP; 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;

  Query Match             91.6%;  Score 3721.4;  DB 5;  Length 3900;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 3731;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy        315 GGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGC 374
              | |  |||  | || |       | ||||||||||||||||||||||||||||||||||
Db        125 GTGCCCCGCTCCCATGTGTCCACAGTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGC 184

Qy        375 AGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGT 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 AGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGT 244

Qy        435 GCTGGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGG 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GCTGGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGG 304

Qy        495 GCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGG 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGG 364

Qy        555 CATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCAC 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 CATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCAC 424

Qy        615 CAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCAT 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 CAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCAT 484

Qy        675 CAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGT 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGT 544

Qy        735 CCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGG 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 CCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGG 604

Qy        795 CTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAA 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 CTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAA 664

Qy        855 GACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGA 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 GACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGA 724

Qy        915 TGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGT 974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 TGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGT 784

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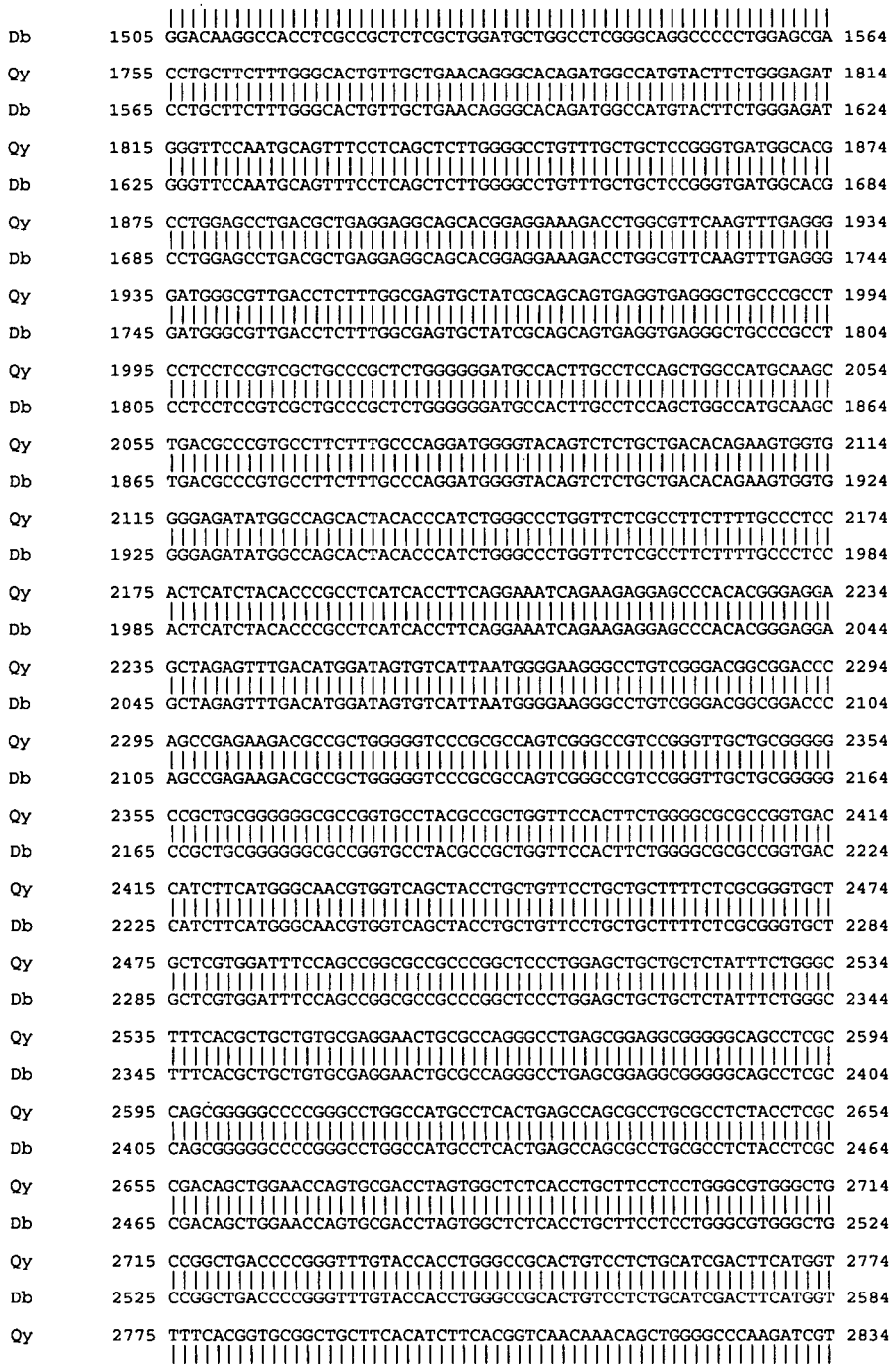
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 1755 CCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGAT 1814
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RESULT 13
ABS58041
ID   ABS58041 standard; cDNA; 3900 BP.
XX
AC   ABS58041;
XX
DT   14-FEB-2003  (first entry)
XX
DE   Human transient receptor potential (TRP)-like calcium channel (TLCC).
XX
KW   Human; gene; ss; transient receptor potential-like calcium channel; TRP;
KW   TLCC; 18607; calcium signalling; growth; differentiation;
KW   capacitative calcium channel; store-operated calcium channel; SOC;
KW   plasma membrane; calcium ion; cytosol; modulator; membrane excitability;
KW   action potential; excitation; neurite outgrowth; synaptogenesis;
KW   signal transduction; angiogenesis; cell proliferation; vascular tone;
KW   gene therapy; diagnosis; cardiovascular disorder; atherosclerosis;
KW   restenosis; endothelial cell disorder; tumour metastasis; psoriasis;
KW   rheumatoid arthritis; diabetes; hepatic disorder; hepatitis; cirrhosis;
KW   central nervous system disorder; Alzheimer's disease;
KW   Parkinson's disease; multiple sclerosis; epilepsy; cancer;
KW   cellular proliferation disorder; migration disorder; therapeutic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag= b
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FT   3'UTR           3391. .3900
FT                   /*tag= c
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PD   03-OCT-2002.
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XX
PR   22-FEB-2000; 2000US-00510706.
PR   31-MAY-2000; 2000US-00583373.
PR   08-AUG-2000; 2000US-00634669.
XX
PA   (GLUC/) GLUCKSMANN M A.
PA   (CURT/) CURTIS R A J.
PA   (LORA/) LORA J M.
XX
PI   Glucksmann MA,  Curtis RAJ,  Lora JM;
XX
DR   WPI; 2003-102516/09.
DR   P-PSDB; ABG72088.
XX
PT   Isolated transient receptor potential-like calcium channel polypeptide,
PT   useful for treating cardiovascular, hepatic, central nervous system
PT   disorders, pain, cellular proliferation, or migration disorder.
XX
PS   Claim 1; Fig 1; 80pp; English.
XX
CC   The invention discloses an isolated transient receptor potential (TRP)-
CC   like calcium channel (TLCC) polypeptide (18607). Calcium signalling has
CC   been implicated in the regulation of a variety of cellular responses,
CC   such as growth and differentiation. TLCC is a member of the capacitative
CC   calcium channel group or store-operated calcium channel (SOC) which is
CC   activated in the plasma membrane to import calcium ions from the
CC   extracellular environment to the cytosol. The nucleic acids, polypeptides
CC   and antibodies of TLCC are useful for detecting its presence in a sample,
CC   for identifying a compound which binds to it and identifying a compound
CC   which modulates its activity. Modulators of TLCC can be used to modulate
CC   membrane excitability, wave forms and frequencies of action potentials,
CC   thresholds of excitation, neurite outgrowth and synaptogenesis, signal
CC   transduction, angiogenesis, endothelial cell proliferation and vascular
CC   tone. The nucleic acid and polypeptide are also useful (using gene
CC   therapy) for diagnosing and treating cardiovascular disorders, such as
CC   atherosclerosis and restenosis, endothelial cell disorders, such as
CC   tumour metastasis, psoriasis, rheumatoid arthritis and diabetes, hepatic
CC   disorders such hepatitis and cirrhosis, central nervous system disorders,
CC   such as Alzheimer's disease, Parkinson's disease, multiple sclerosis and
CC   epilepsy, cellular proliferation disorders, such as cancer, and growth,
CC   differentiation or migration disorders. TLCC can also be used in
CC   predictive medicine (e.g. diagnostic assays, prognostic assays,
CC   monitoring clinical trials and pharmacogenomics) and in methods of
CC   treatment (e.g. therapeutic and prophylactic). The sequence presented is
CC   the human TLCC, 18607, cDNA
XX
SQ   Sequence 3900 BP; 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;

  Query Match             91.6%;  Score 3721.4;  DB 8;  Length 3900;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 3731;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy        315 GGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGC 374
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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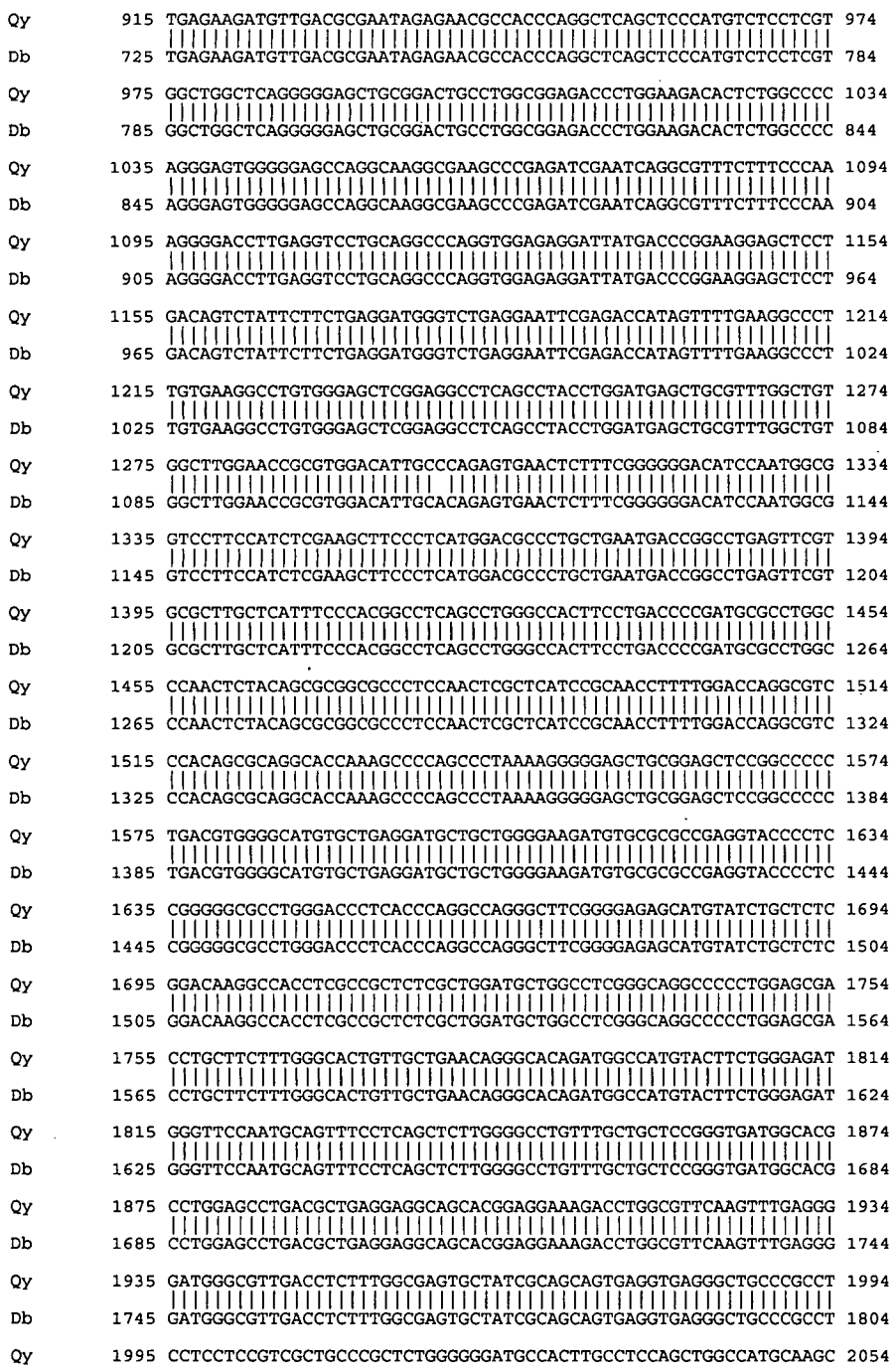
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGT 544

Qy        735 CCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGG 794
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 2115 GGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCC 2174
Db 1925 GGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCC 1984
Qy 2175 ACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGA 2234
Db 1985 ACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGA 2044
Qy 2235 GCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCC 2294
Db 2045 GCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCC 2104
Qy 2295 AGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGG 2354
Db 2105 AGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGG 2164
Qy 2355 CCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGAC 2414
Db 2165 CCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGAC 2224
Qy 2415 CATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCT 2474
Db 2225 CATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCT 2284
Qy 2475 GCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGC 2534
Db 2285 GCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGC 2344
Qy 2535 TTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGC 2594
Db 2345 TTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGC 2404
Qy 2595 CAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGC 2654
Db 2405 CAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGC 2464
Qy 2655 CGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTG 2714
Db 2465 CGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTG 2524
Qy 2715 CCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGT 2774
Db 2525 CCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGT 2584
Qy 2775 TTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGT 2834
Db 2585 TTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGT 2644
Qy 2835 CATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCT 2894
Db 2645 CATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCT 2704
Qy 2895 GGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAG 2954
Db 2705 GGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAG 2764
Qy 2955 TATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGA 3014
Db 2765 TATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGA 2824
Qy 3015 GGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGC 3074
Db 2825 GGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGC 2884
Qy 3075 ACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGT 3134

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Db       2885 ACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGT 2944

Qy       3135 GCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGC 3194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2945 GCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGC 3004

Qy       3195 CATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCA 3254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3005 CATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCA 3064

Qy       3255 GCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGT 3314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3065 GCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGT 3124

Qy       3315 CATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCC 3374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3125 CATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCC 3184

Qy       3375 GTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCT 3434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3185 GTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCT 3244

Qy       3435 GCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCG 3494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3245 GCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCG 3304

Qy       3495 GGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACA 3554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3305 GGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACA 3364

Qy       3555 GCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCA 3614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3365 GCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCA 3424

Qy       3615 GTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCC 3674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3425 GTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCC 3484

Qy       3675 AGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTT 3734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3485 AGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTT 3544

Qy       3735 CAAGGAGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCC 3794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3545 CAAGGAGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCC 3604

Qy       3795 CCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGG 3854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3605 CCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGG 3664

Qy       3855 ACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAG 3914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3665 ACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAG 3724

Qy       3915 TCCCAGCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGG 3974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3725 TCCCAGCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGG 3784

Qy       3975 GTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGA 4034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3785 GTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGA 3844

Qy       4035 AATAAAGCCATTTCAGAGGAAAAAAAA 4061
              ||||||||||||||||||||||||||||
Db       3845 AATAAAGCCATTTCAGAGGAAAAAAAA 3871


RESULT 14
ADH51622
ID   ADH51622 standard; cDNA; 3900 BP.
XX
AC   ADH51622;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human 18607 protein cDNA sequence.
XX
KW   cytostatic; vasotropic; haemostatic; nephrotropic; gastrointestinal-Gen;
KW   respiratory-Gen; muscular-Gen; osteopathic; antiinflammatory;
KW   immunosuppressive; cardiovascular-Gen; hepatotropic; virucide; analgesic;
KW   antianaemic; endocrine-Gen; neuroprotective; nootropic; cardiant;
KW   gene therapy; cellular proliferative; differentiative disorder; brain;
KW   blood vessel; platelet; breast; colon; kidney; lung; ovarian; prostate;
KW   pancreatic; skeletal muscle; testicular; hormonal; bone metabolism;
KW   immune disorder; inflammatory disorder; cardiovascular disorder;
KW   endothelial cell; liver; viral; pain; metabolic; anaemia; angiogenesic;
KW   neoplastic; endocrine disorder; neurological; heart; tissue typing;
KW   chromosomal mapping; predictive medicine; pharmacogenomic; human; gene;
KW   ss; 18607.
XX
OS   Homo sapiens.
XX
PN   US2003219806-A1.
XX
PD   27-NOV-2003.
XX
PF   18-MAR-2003; 2003US-00391399.
XX
PR   22-FEB-2000; 2000US-00510706.
PR   07-APR-2000; 2000US-0195734P.
PR   31-MAY-2000; 2000US-00583373.
PR   26-JUN-2000; 2000US-0214176P.
PR   08-AUG-2000; 2000US-00634669.
PR   31-AUG-2000; 2000US-0229036P.
PR   19-SEP-2000; 2000US-0233537P.
PR   01-FEB-2001; 2001US-0267076P.
PR   20-FEB-2001; 2001US-00789481.
PR   12-MAR-2001; 2001US-0275078P.
PR   12-MAR-2001; 2001US-0275172P.
PR   06-APR-2001; 2001US-00828035.
PR   26-JUN-2001; 2001US-00891762.
PR   29-AUG-2001; 2001US-00942447.
PR   17-SEP-2001; 2001US-0322983P.
PR   19-SEP-2001; 2001US-00957683.
PR   27-SEP-2001; 2001US-0325854P.
PR   04-DEC-2001; 2001US-0336936P.
PR   31-JAN-2002; 2002US-00062937.
PR   08-MAR-2002; 2002US-00094214.
PR   11-MAR-2002; 2002US-00095139.
PR   17-SEP-2002; 2002US-00245121.
PR   26-SEP-2002; 2002US-00255532.
PR   04-DEC-2002; 2002US-00309804.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Glucksmann MA,  Curtis RAJ,  Lora JM,  Galvin KM,  Silos-Santiago I;
XX
DR   WPI; 2004-010868/01.
DR   P-PSDB; ADH51623.
XX
PT   New 18607, 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324,
PT   55063, 52991, 59914, 59921 or 33751 nucleic acid molecule or polypeptide,
PT   useful for diagnosing, preventing or treating e.g. proliferative or brain
PT   disorders.
XX
PS   Claim 1; SEQ ID NO 1; 276pp; English.
XX
CC   This invention relates to novel human DNA sequences (designated 18607,
CC   15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324, 55063,
CC   52991, 59914, 59921 or 33751) and the proteins encoded by them. The
CC   invention may be useful for the development of compounds with a
CC   cytostatic, vasotropic, haemostatic, nephrotropic, gastrointestinal-Gen,
CC   respiratory-Gen, muscular-Gen, osteopathic, antiinflammatory,
CC   immunosuppressive, cardiovascular-Gen, hepatotropic, virucide, analgesic,
CC   antianaemic, endocrine-Gen, neuroprotective, nootropic or cardiant
CC   activity. In addition, the sequences may be useful for gene therapy. The
```

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CC   invention may be useful in diagnosing, preventing or treating disorders
CC   characterised by aberrant 18607, 15603, 69318, 12303, 48000, 52920, 5433,
CC   38554, 57301, 58324, 55063, 52991, 59914, 59921 or 33751 activity, for
CC   example cellular proliferative and/or differentiative disorder, brain
CC   disorder, blood vessel disorder, platelet disorder, breast disorder,
CC   colon disorder, kidney disorder, lung disorder, ovarian disorder,
CC   prostate disorder, pancreatic disorder, skeletal muscle disorder,
CC   testicular disorder, hormonal disorder, disorder associated with bone
CC   metabolism, immune disorder, inflammatory disorder, cardiovascular
CC   disorder, endothelial cell disorder, liver disorder, viral disease, pain,
CC   metabolic disorder, anaemia, angiogenesic disorder, neoplastic disorder,
CC   endocrine disorder, neurological disorder or heart disorder. They may
CC   also be used in screening assays, tissue typing, chromosomal mapping,
CC   predictive medicine or pharmacogenomics. The present sequence is that of
CC   the cDNA which encodes the human 18607 protein of the invention.
XX
SQ   Sequence 3900 BP; 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;

  Query Match             91.6%;  Score 3721.4;  DB 12;  Length 3900;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 3731;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy        315 GGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGC 374
              |  |  |||  |  ||  |      | ||||||||||||||||||||||||||||||||||
Db        125 GTGCCCCGCTCCCATGTGTCCACAGTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGC 184

Qy        375 AGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGT 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 AGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGT 244

Qy        435 GCTGGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGG 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GCTGGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGG 304

Qy        495 GCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGG 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGG 364

Qy        555 CATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCAC 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 CATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCAC 424

Qy        615 CAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCAT 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 CAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCAT 484

Qy        675 CAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGT 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGT 544

Qy        735 CCAGTTTCCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGG 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 CCAGTTTCCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGG 604

Qy        795 CTGCCTGGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAA 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 CTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAA 664

Qy        855 GACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGA 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 GACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGA 724

Qy        915 TGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGT 974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 TGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGT 784

Qy        975 GGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCC 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        785 GGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCC 844

Qy       1035 AGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAA 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        845 AGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAA 904

Qy       1095 AGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCT 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         905 AGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCT 964

Qy       1155 GACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCT 1214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         965 GACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCT 1024

Qy       1215 TGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGT 1274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1025 TGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGT 1084

Qy       1275 GGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCG 1334
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        1085 GGCTTGGAACCGCGTGGACATTGCACAGAGTGAACTCTTTCGGGGGGACATCCAATGGCG 1144

Qy       1335 GTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGT 1394
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1145 GTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGT 1204

Qy       1395 GCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGC 1454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1205 GCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGC 1264

Qy       1455 CCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTC 1514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1265 CCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTC 1324

Qy       1515 CCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCC 1574
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1325 CCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCC 1384

Qy       1575 TGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTC 1634
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1385 TGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTC 1444

Qy       1635 CGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTC 1694
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Db        1445 CGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTC 1504

Qy       1695 GGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGA 1754
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1505 GGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGA 1564

Qy       1755 CCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGAT 1814
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1565 CCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGAT 1624

Qy       1815 GGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACG 1874
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Db        1625 GGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACG 1684

Qy       1875 CCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGG 1934
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1685 CCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGG 1744

Qy       1935 GATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCT 1994
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1745 GATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCT 1804

Qy       1995 CCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGC 2054
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1805 CCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGC 1864

Qy       2055 TGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTG 2114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1865 TGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTG 1924

Qy       2115 GGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCC 2174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1925 GGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCC 1984
```

```
Qy       2175 ACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGA 2234
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1985 ACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGA 2044

Qy       2235 GCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCC 2294
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2045 GCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCC 2104

Qy       2295 AGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGG 2354
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2105 AGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGG 2164

Qy       2355 CCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGAC 2414
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2165 CCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGAC 2224

Qy       2415 CATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCT 2474
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2225 CATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCT 2284

Qy       2475 GCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGC 2534
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2285 GCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGC 2344

Qy       2535 TTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGC 2594
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2345 TTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGC 2404

Qy       2595 CAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGC 2654
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2405 CAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGC 2464

Qy       2655 CGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTG 2714
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2465 CGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTG 2524

Qy       2715 CCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGT 2774
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Db       2525 CCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGT 2584

Qy       2775 TTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGT 2834
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Db       2585 TTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGT 2644

Qy       2835 CATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCT 2894
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2645 CATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCT 2704

Qy       2895 GGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAG 2954
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2955 TATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGA 3014
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Db       2765 TATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGA 2824

Qy       3015 GGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGC 3074
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Qy       3075 ACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGT 3134
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Db       2885 ACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGT 2944

Qy       3135 GCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGC 3194
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Qy       3195 CATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCA 3254
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Db       3005 CATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCA 3064

Qy       3255 GCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGT 3314
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Qy       3315 CATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCC 3374
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3375 GTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCT 3434
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Db       3185 GTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCT 3244

Qy       3435 GCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCG 3494
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Qy       3495 GGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACA 3554
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Qy       3615 GTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCC 3674
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Qy       3675 AGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTT 3734
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Db       3485 AGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTT 3544

Qy       3735 CAAGGAGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCC 3794
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Db       3545 CAAGGAGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCC 3604

Qy       3795 CCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGG 3854
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3605 CCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGG 3664

Qy       3855 ACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAG 3914
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3665 ACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAG 3724

Qy       3915 TCCCAGCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGG 3974
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3725 TCCCAGCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGG 3784

Qy       3975 GTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGA 4034
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Qy       4035 AATAAAGCCATTTCAGAGGAAAAAAAA 4061
             ||||||||||||||||||||||||||||
Db       3845 AATAAAGCCATTTCAGAGGAAAAAAAA 3871
```

RESULT 15
ABK28677
ID ABK28677 standard; cDNA; 3599 BP.
XX
AC ABK28677;
XX
DT 09-APR-2002 (first entry)
XX
DE Human cDNA encoding secreted potein SECP44.
XX
KW Human; ss; gene; SECP; antiinflammatory; cytostatic; cardiant;
KW immunosuppressive; antiviral; anti-HIV; antiarthritic; antirheumatic;
KW muscular active general; anticonvulsant; nootropic; neuroprotective;
KW antiallergic; hypotensive; cardiovascular disorder; atherosclerosis;
KW hypertension; myocardial infarction; autoimmune disorder;
KW inflammatory disorder; AIDS; acquired immunodeficiency syndrome; allergy;
KW rheumatoid arthritis; cell proliferative disorder; cancer;

```
KW   developmental disorder; Duchenne muscular dystrophy;
KW   neurological disorder; epilepsy; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO200198353-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US019862.
XX
PR   20-JUN-2000; 2000US-0212890P.
PR   23-JUN-2000; 2000US-0213466P.
PR   27-JUN-2000; 2000US-0214601P.
PR   31-JUL-2000; 2000US-0222372P.
PR   08-SEP-2000; 2000US-0231435P.
PR   15-SEP-2000; 2000US-0232889P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Hillman JL,  Tang YT,  Yue H,  Elliott VS,  Tribouley CM,  Lee EA;
PI   Ramkumar J,  Lal P,  Xu Y,  Warren BA,  Hafalia AJA,  Baughn MR;
PI   Azimzai Y,  Batra S,  Burford N,  Yao MG,  Nguyen DB,  Lu DAM,  Walia NK;
PI   Gandhi AR,  Au-Young J,  Patterson C;
XX
DR   WPI; 2002-090431/12.
DR   P-PSDB; AAU82018.
XX
PT   Forty four human secreted proteins (referred to as SECP-1 to SECP-44),
PT   useful in the diagnosis, treatment and prevention of cardiovascular (e.g.
PT   atherosclerosis), autoimmune/inflammatory (e.g. allergies) and cell
PT   proliferative disorders.
XX
PS   Claim 5; Page 195; 195pp; English.
XX
CC   The invention relates to forty four human secreted proteins (referred to
CC   as SECP-1 to SECP-44) and the nucleic acids encoding them. Also included
CC   are a host cell transformed with the nucleic acid, a transgenic animal
CC   comprising the nucleic acid, an anti-SECP antibody, use of the SECP
CC   proteins in isolating agonists and antagonists of SECP activity and a
CC   method of isolating compounds which alter the expression of the SECP
CC   nucleic acid. The SECP polynucleotides and polypeptides are useful in the
CC   diagnosis, treatment and prevention of cardiovascular (e.g.
CC   atherosclerosis, hypertension, myocardial infarction),
CC   autoimmune/inflammatory (e.g. acquired immunodeficiency syndrome (AIDS),
CC   allergies, rheumatoid arthritis), cell proliferative (e.g. cancer),
CC   developmental (e.g. Duchenne and Becker muscular dystrophy), and
CC   neurological (e.g. epilepsy, Alzheimer's disease) disorders. Numerous
CC   other examples of each disorder are given in the specification. The
CC   present sequence is a cDNA encoding a SECP protein
XX
SQ   Sequence 3599 BP; 602 A; 1137 C; 1139 G; 721 T; 0 U; 0 Other;

  Query Match             88.2%;  Score 3579.8;  DB 6;  Length 3599;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3592;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy        449 GGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTG 508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTG 60

Qy        509 CCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATG 568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        569 TTGGTGTG-GCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCC 627
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Db        121 TTGGTGTGCGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCC 180

Qy        628 ATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGC 687
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTG 300

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        808 GAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGA 867
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGA 420

Qy        868 GGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTG 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        928 ACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGG 987
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Qy        988 GGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGA 1047
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGA 600

Qy       1048 GCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAG 1107
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Qy       1108 GTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCT 1167
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Db        661 GTCCTTCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCT 720

Qy       1168 TCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGT 1227
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Db        721 TCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGT 780

Qy       1228 GGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGC 1287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGC 840

Qy       1288 GTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTC 1347
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Db        841 GTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTC 900

Qy       1348 GAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATT 1407
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Qy       1408 TCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGC 1467
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Db        961 TCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGC 1020

Qy       1468 GCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGC 1527
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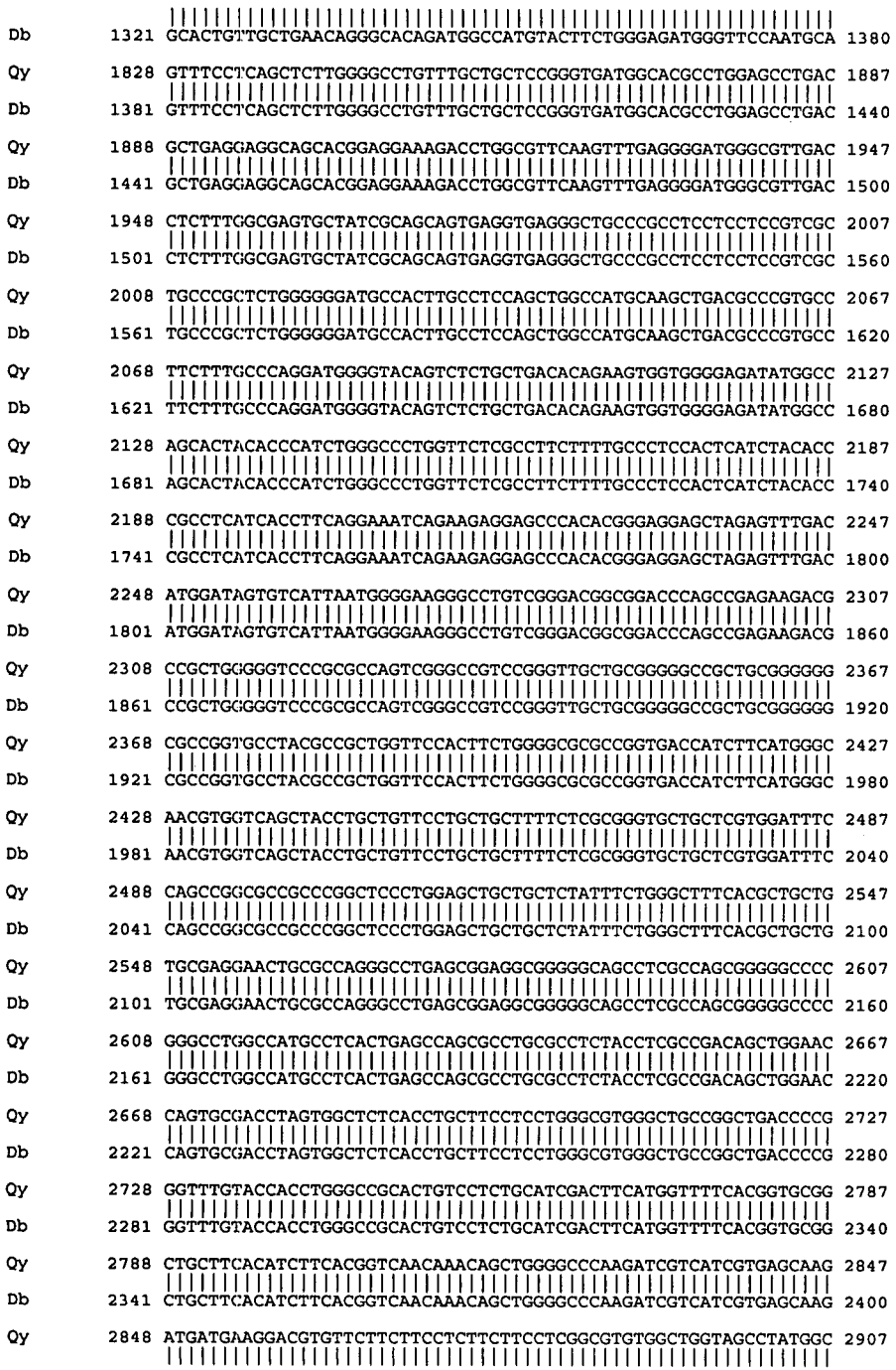
Qy       1528 ACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCAT 1587
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCAT 1140

Qy       1588 GTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGG 1647
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1648 GACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACC 1707
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACC 1260

Qy       1708 TCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGG 1767
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Db       1261 TCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGG 1320

Qy       1768 GCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCA 1827
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Db 1321 GCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCA 1380
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Db 1381 GTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGAC 1440
Qy 1888 GCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGAC 1947
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Qy 1948 CTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGC 2007
Db 1501 CTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGC 1560
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Db 1801 ATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACG 1860
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Qy 2428 AACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTC 2487
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Qy 2548 TGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCC 2607
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Qy 2608 GGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAAC 2667
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Db 2221 CAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCG 2280
Qy 2728 GGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGG 2787
Db 2281 GGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGG 2340
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Db 2401 ATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGC 2460
Qy 2908 GTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGC 2967
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Search completed: June 12, 2005, 18:59:27
Job time : 1366.41 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 16:55:33 ; Search time 8319.65 Seconds
(without alignments)
18579.996 Million cell updates/sec

Title: US-09-869-486B-29
Perfect score: 4061
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
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6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	773.6	19.0	912	6	CA488162	CA488162 AGENCOURT
c	3	724	17.8	734	6	CA312705	CA312705 UI-CF-FN0
c	4	721.4	17.8	733	5	BU687299	BU687299 UI-CF-EC1
	5	719	17.7	879	5	BU858032	BU858032 AGENCOURT
	6	712.2	17.5	774	4	BG759687	BG759687 602713380
	7	697.4	17.2	700	7	CN402549	CN402549 170004706
	8	690	17.0	933	5	BQ942718	BQ942718 AGENCOURT
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ALIGNMENTS

RESULT 1
AK044094
LOCUS AK044094 4293 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830089H13 product:similar to TRP-RELATED CATION INFLUX CHANNEL [Homo sapiens], full insert sequence.
ACCESSION AK044094
VERSION AK044094.1 GI:26336171
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research

```
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 4293)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
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ORIGIN

  Query Match             49.6%;  Score 2016.2;  DB 3;  Length 4293;
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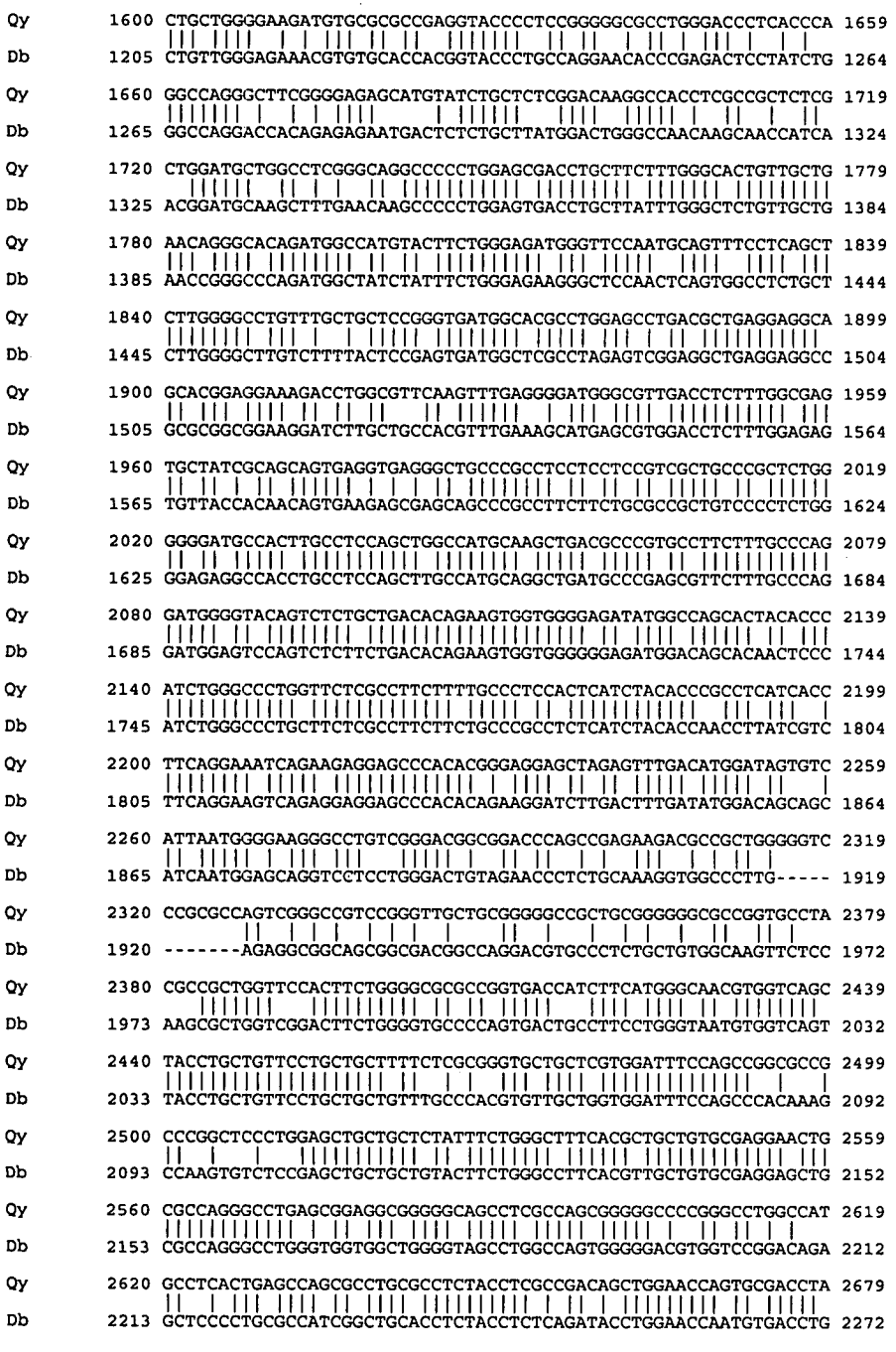
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Qy 2980 CCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAG 3039
Db 2573 CCGTATCTGCAGATCTTCGGACAAATTCCCCAGGAGGAAATGGACGTGGCCCTCATGATT 2632
Qy 3040 CACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGC 3099
Db 2633 CCAGGTAACTGCTCAATGGAGCGGGGCTCCTGGGCTCATCCGGAGGGGCCCGTCGCAGGC 2692
Qy 3100 ACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTGCTC 3159
Db 2693 TCCTGTGTGTCCCAGTATGCCAACTGGCTGGTGGTGTTGCTCCTTATCGTCTTCTTGCTG 2752
Qy 3160 GTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGCAAA 3219
Db 2753 GTGGCCAATATCCTGTTGCTCAACCTGCTCATCGCCATGTTCAGCTACACCTTCAGCAAA 2812
Qy 3220 GTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTC 3279
Db 2813 GTGCACGGCAACAGCGACCTCTACTGGAAGGCACAGCGCTACAGCCTCATCCGGGAATTC 2872
Qy 3280 CACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTC 3339
Db 2873 CATTCGAGGCCTGCCCTGGCCCCACCCCTCATCATCATCTGTCA---------- 2916
Qy 3340 AGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTTC 3399
Db 2917 ---------- 2916
Qy 3400 CGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAG 3459
Db 2917 TGTGTCTGTCTCTGTAAGGAAGCAGAGCGGAAGCTGCTGACTTGGGAGTCTGTGCACAAA 2976
Qy 3460 GAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAG 3519
Db 2977 GAGAACTTCCTGTTGGCACAAGCTCGGGACAAGCGAGACAGTGACTCGGAGCGTTTGAAA 3036
Qy 3520 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAA 3579
Db 3037 CGCACGTCTCAGAAGGTGGACACTGCACTGAAGCAGCTGGGACAGATCAGAGAGTACGAT 3096
Qy 3580 CAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTG 3639
Db 3097 CGGCGTCTGAGGGGGCTGGAGAGAGAGGTCCAACACTGTTCTCGAGTCCTGACTTGGATG 3156
Qy 3640 GCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTG 3699
Db 3157 GCTGAGGCCCTTAGCCACTCTGCCTTGCTGCCTCCAGGGGCCCCACCCCCTCCGAGCCCC 3216
Qy 3700 CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATT 3759
Db 3217 ACTGGTTCCAAAGACTGAGTGTTCCTGGTGGATGTGTAGGTGTTTGCATCCAGAGAGGGT 3276
Qy 3760 TTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTG 3819

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Db       3277 TCATTCCTCAAGCTGGGCCCA-GTCTGCCTCAAGCGACACAACTGGTGGCCTTATCCTCA 3335

Qy       3820 AGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTC---ATCC 3876

Db       3336 CCACGAATCCCATG--CTTATGGGTTGCTGTCCAGACACACTGCGAGTATCACCGAGGGA 3393

Qy       3877 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 3936

Db       3394 CTCCTTCCCAGAGCAGCCTCACCTTGGGTGAATCAAGCTCTGAGCTGGCAAAGTTGGCCT 3453

Qy       3937 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 3996

Db       3454 CTTTGTGGGCCCAGCCACACAGCAGAGGAAGCAGGAGGGTCCT--GGGGTGCAGGAACCA 3511

Qy       3997 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCA 4049

Db       3512 CAGACC-----CTACACACAGCTTCCCCACAATGGGGAAATAAAACCATTTGA 3559


RESULT 2
CA488162
LOCUS       CA488162                912 bp    mRNA    linear   EST 14-NOV-2002
DEFINITION  AGENCOURT_10808068 MAPcL Homo sapiens cDNA clone IMAGE:6719903 5',
            mRNA sequence.
ACCESSION   CA488162
VERSION     CA488162.1  GI:24949318
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 912)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Kristi A. Egland, Ira Pastan
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14278  row: i  column: 23
            High quality sequence start: 28
            High quality sequence stop: 728.
FEATURES             Location/Qualifiers
     source          1. .912
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6719903"
                     /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
                     hTERT-HME1, LNCaP"
                     /lab_host="EMDH10B"
                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification:  26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee  & Ira Pastan:  Discovery of new breast
                     cancer genes encoding  membrane and secreted proteins.
                     Manuscript submitted."
ORIGIN

  Query Match             19.0%;  Score 773.6;  DB 6;  Length 912;
  Best Local Similarity   94.3%;  Pred. No. 2.4e-156;
  Matches  812;  Conservative    0;  Mismatches   47;  Indels    2;  Gaps    1;

Qy       2850 GATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGT 2909

Db         46 GATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGT 105

Qy       2910 GGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGT 2969

Db        106 GGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGT 165

Qy       2970 CTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGC 3029

Db        166 CTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGC 225

Qy       3030 CCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGC 3089

Db        226 CCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGC 285

Qy       3090 CCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCAT 3149

Db        286 CCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCAT 345

Qy       3150 CTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACAC 3209

Db        346 CTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACAC 405

Qy       3210 ATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCAT 3269

Db        406 ATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCAT 465

Qy       3270 CCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCG 3329

Db        466 CCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCG 525

Qy       3330 CCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCT 3389

Db        526 CCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCT 585

Qy       3390 CGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATC 3449

Db        586 CGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATC 645

Qy       3450 GGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGA 3509

Db        646 GGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGA 705

Qy       3510 GCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCG 3569

Db        706 GCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCG 765

Qy       3570 CGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCC--GCGTC 3627

Db        766 CGAGTACGAACAGCGCCCTGAAGTGCTGGAGCGGGAGGTCCAGCAGTGTACGCGGGCCTC 825

Qy       3628 CTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCA 3687

Db        826 CGGGGGGTGGTTNNTCCNCTCCCTCTCCCCTCCCCCTCCCTTCCCCTCCCCTCTCTCTCC 885

Qy       3688 CCCCCTGACCTGCCTGGGTCC 3708

Db        886 CCCCCTCCCCGCCCCCGCTCC 906


RESULT 3
CA312705/c
LOCUS       CA312705                734 bp    mRNA    linear   EST 04-NOV-2002
DEFINITION  UI-CF-FN0-afl-c-16-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
            UI-CF-FN0-afl-c-16-0-UI 3', mRNA sequence.
ACCESSION   CA312705
VERSION     CA312705.1  GI:24530803
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 734)
```

```
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .734
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-FN0-afl-c-16-0-UI"
                     /tissue_type="Human Lung Epithelial cells"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-FN0"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-FN0 is a subtracted cDNA library derived from two
                     normalized Human lung epithelial cell libraries (EN1 and
                     DU1) The library was subtracted according to according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. For additional information, contact:
                     bento-soares@uiowa.edu
                     TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
                     6hr to LPS 24h
                     TAG_LIB=UI-CF-FN0
                     TAG_SEQ=CTGCTCAGGT"
ORIGIN

  Query Match             17.8%;  Score 724;  DB 6;  Length 734;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-145;
  Matches  724;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3338 TCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATT 3397
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Db        734 TCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATT 675

Qy       3398 TCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATA 3457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 TCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATA 615

Qy       3458 AGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGA 3517
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 AGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGA 555

Qy       3518 AGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACG 3577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 AGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACG 495

Qy       3578 AACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGG 3637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGG 435

Qy       3638 TGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACC 3697
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Db        434 TGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACC 375

Qy       3698 TGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGA 3757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 TGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGA 315

Qy       3758 TTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCT 3817
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Db        314 TTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCT 255

Qy       3818 TGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCT 3877
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Db        254 TGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCT 195

Qy       3878 TACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGC 3937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 TACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGC 135

Qy       3938 CTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCAC 3997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 CTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCAC 75

Qy       3998 AGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAAA 4057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          74 AGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAAA 15

Qy       4058 AAAA 4061
             ||||
Db          14 AAAA 11


RESULT 4
BU687299/c
LOCUS       BU687299                733 bp    mRNA    linear   EST 07-OCT-2002
DEFINITION  UI-CF-EC1-adv-g-20-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
            UI-CF-EC1-adv-g-20-0-UI 3', mRNA sequence.
ACCESSION   BU687299
VERSION     BU687299.1  GI:23543033
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 733)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .733
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EC1-adv-g-20-0-UI"
                     /tissue_type="Lung"
                     /dev_stage="Adult and Fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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/clone_lib="UI-CF-EC1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGCTTAC.
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"

ORIGIN

Query Match 17.8%; Score 721.4; DB 5; Length 733;
Best Local Similarity 99.9%; Pred. No. 4.5e-145;
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db        733 CAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCATTT 674

Qy       3399 CCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAA 3458
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Db        673 CCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAA 614

Qy       3459 GGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAA 3518
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Db        613 GGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAA 554

Qy       3519 GCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGA 3578
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Db        553 GCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGA 494

Qy       3579 ACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGT 3638
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Db        493 ACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGT 434

Qy       3639 GGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCT 3698
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Db        433 GGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCT 374

Qy       3699 GCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGAT 3758
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Db        373 GCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGAT 314

Qy       3759 TTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTT 3818
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Db        313 TTTGCTCCTAGAGTAAGGCTCATTTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTT 254

Qy       3819 GAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTT 3878
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Db        253 GAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTT 194

Qy       3879 ACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCC 3938
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Db        193 ACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCC 134

Qy       3939 TGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACA 3998
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Db        133 TGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACA 74

Qy       3999 GACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAAAA 4058
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Qy       4059 AAA 4061
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Db         13 AAA 11
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RESULT 5
BU858032
LOCUS BU858032 879 bp mRNA linear EST 16-OCT-2002
DEFINITION AGENCOURT_10478874 NIH_MGC_107 Homo sapiens cDNA clone IMAGE:6647959 5', mRNA sequence.
ACCESSION BU858032
VERSION BU858032.1 GI:24043024
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 879)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2889 row: d column: 07
High quality sequence start: 11
High quality sequence stop: 612.
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source 1. .879
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_107"
/note="Organ: breast; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 17.7%; Score 719; DB 5; Length 879;
Best Local Similarity 96.6%; Pred. No. 1.5e-144;
Matches 799; Conservative 0; Mismatches 20; Indels 8; Gaps 6;

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Qy       2412 GACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGT 2471
             ||||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACCATCTTCATGGGCTACCTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGT 60

Qy       2472 GCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTG 2531
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTG 120

Qy       2532 GGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCT 2591
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCT 180

Qy       2592 CGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCT 2651
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCT 240
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Qy       2652 CGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGG 2711
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGG 300

Qy       2712 CTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCAT 2771
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Db        301 CTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCAT 360

Qy       2772 GGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGAT 2831
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Db        361 GGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGAT 420

Qy       2832 CGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTG 2891
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Db        421 CGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTG 480

Qy       2892 GCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCC 2951
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Db        481 GCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCC 540

Qy       2952 AAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCA 3011
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Db        541 AAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCA 600

Qy       3012 GGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCC-GGCTTCT 3070
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Db        601 GGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGGCTTCT 660

Qy       3071 GGGCACACCCTCCTGGGG-CCCAGGCGGGCACCTGCG-TCTCCCAGTATGCCAACT-GGC 3127
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Db        661 GGGCACACCCTCCTGGGGCCCCAGCGGGGCACCTGCGNTCTCCCAGTATGCCCACTGGGC 720

Qy       3128 TGGTGGTGCTGC-TCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTG 3186
             |||||||||||| ||| || ||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGTGGTGCTGCTTCCCCGCCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTG 780

Qy       3187 CTCATTGCCATGTTCAGTTACACA---TTCGGCAAAGTACAGGGCAA 3230
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Db        781 CTCATTGCCAATGTTCAGTTAACACATTCCGCCAAAGTACCGGGCCA 827
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RESULT 6
BG759687
LOCUS BG759687 774 bp mRNA linear EST 15-MAY-2001
DEFINITION 602713380F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853634 5', mRNA sequence.
ACCESSION BG759687
VERSION BG759687.1 GI:14070340
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 774)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1699 row: p column: 19
High quality sequence stop: 711.
FEATURES Location/Qualifiers
source 1. .774
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4853634"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 17.5%; Score 712.2; DB 4; Length 774;
Best Local Similarity 99.6%; Pred. No. 4.4e-143;
Matches 714; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       3320 CCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCT 3379
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Db          2 CCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCT 61

Qy       3380 CCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAA 3439
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Db         62 CCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAA 121

Qy       3440 CGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGA 3499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGA 181

Qy       3500 GCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGG 3559
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Db        182 GCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGG 241

Qy       3560 GACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA 3619
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Db        242 GACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA 301

Qy       3620 GCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTG 3679
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Db        302 GCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTG 361

Qy       3680 GGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGG 3739
             ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GGCCTGCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGG 421

Qy       3740 AGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGC 3799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 AGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGC 481

Qy       3800 ACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCAC 3859
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Db        482 ACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCAC 541

Qy       3860 CTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCA 3919
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Db        542 CTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCA 601

Qy       3920 GCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCT 3979
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 GCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCT 661

Qy       3980 TGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAA 4036
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        662 TGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATTCCTCACACTGCGGAAA 718
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RESULT 7
CN402549
LOCUS CN402549 700 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000470662623 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN402549

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VERSION     CN402549.1  GI:47390143
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 700)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 700   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .700
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, cell lines H1, H7, and
                     H9"
                     /clone_lib="GRN_ES"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from undifferentiated hES cell lines H1 (p32), H7 (p29),
                     and H9 (p26) maintained in feeder-free conditions"
ORIGIN

  Query Match             17.2%;  Score 697.4;  DB 7;  Length 700;
  Best Local Similarity   99.9%;  Pred. No. 6.9e-140;
  Matches  698;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        370 GCTGCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTG 429
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Db          2 GCTGCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTG 61

Qy        430 TCAGTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGT 489
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Db         62 TCAGTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGT 121

Qy        490 CGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCAC 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCAC 181

Qy        550 ACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGG 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 ACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGG 241

Qy        610 GGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACC 301

Qy        670 CTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGAC 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGAC 361

Qy        730 GGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACA 789
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Db        362 GGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACA 421

Qy        790 CACGGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAG 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 CACGGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAG 481

Qy        850 CAGAAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGAT 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 CAGAAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGAT 541

Qy        910 GGTGATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTC 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GGTGATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTC 601

Qy        970 CTCGTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTG 1029
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        602 CTCGTGGCTGGCTCAAGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTG 661

Qy       1030 GCCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGA 1068
              ||||||||||||||||||||||||||||||||||||||||
Db        662 GCCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGA 700


RESULT 8
BQ942718
LOCUS       BQ942718                933 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT_8842138 Lupski_sciatic_nerve Homo sapiens cDNA clone
            IMAGE:6204319 5', mRNA sequence.
ACCESSION   BQ942718
VERSION     BQ942718.1  GI:22358196
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 933)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13625  row: g  column: 08
            High quality sequence stop: 501.
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                     /tissue_type="sciatic nerve"
                     /dev_stage="adult, 70 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_sciatic_nerve"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.87 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
ORIGIN

  Query Match             17.0%;  Score 690;  DB 5;  Length 933;
  Best Local Similarity   92.3%;  Pred. No. 2.9e-138;
  Matches  783;  Conservative    0;  Mismatches   55;  Indels   10;  Gaps    5;

Qy       1489 ATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAA 1548
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Db          4 ATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAA 63

Qy       1549 GGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGG 1608
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Db        64 GGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGG 123

Qy      1609 AAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGC 1668
Db       124 AAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGC 183

Qy      1669 TTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCT 1728
Db       184 TTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCT 243

Qy      1729 GGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCA 1788
Db       244 GGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCA 303

Qy      1789 CAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCC 1848
Db       304 CAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCC 363

Qy      1849 TGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGG 1908
Db       364 TGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGG 423

Qy      1909 AAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGC 1968
Db       424 AAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGC 483

Qy      1969 AGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCC 2028
Db       484 AGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCC 543

Qy      2029 ACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTA 2088
Db       544 ACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAAGATGGGGTA 603

Qy      2089 CAGTCTCTGCTGACACAGAAGTGGT-GGGGAGATATGGCCAGCACTACACCCATCTGGGC 2147
Db       604 CAGCCTCTGCTGACACAGAAGTGGTGGGGGAGATATGGCCAGCACTACACCCATCTGGGC 663

Qy      2148 CCTGGTTCT-CGCCTTCTTTTGCCCTCCACTCATCTACACCCGCC--TCATCACCTTCAG 2204
Db       664 CCTGGTTTTCCGCCTTCTTTTGCCCTCCACTCTTCTACCCCCGCCCTTCATTACCTTCCG 723

Qy      2205 GAAATCAGAAGAGGAGCCCACAC---GGGAGGAGCTAGAGTTTGACATGGATAGTGTCAT 2261
Db       724 GAAATCAGAAAGAGGACCCCCCCCCGGGAGGGAGTTGAGTTTGAACTGGGACAGTGGCTT 783

Qy      2262 TAATGGGGAAGGG---CCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGT 2318
Db       784 TCATGGGGGAAGGGCCTCGCCTGGAAGGTGGGACCGTTCCACAGGGACCCCCGTTGGGGC 843

Qy      2319 CCCGCGCC 2326
Db       844 CGCTCGCC 851


RESULT 9
BQ721564
LOCUS       BQ721564                894 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8234684 Lupski_sympathetic_trunk Homo sapiens cDNA clone
            IMAGE:6188589 5', mRNA sequence.
ACCESSION   BQ721564
VERSION     BQ721564.1  GI:21860461
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 894)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13584  row: g  column: 22
            High quality sequence stop: 500.
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                     /dev_stage="adult, 16 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_sympathetic_trunk"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.9 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine); available through Life
                     Technologies."
ORIGIN
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Query Match 16.4%; Score 666; DB 5; Length 894;
Best Local Similarity 97.3%; Pred. No. 4.4e-133;
Matches 720; Conservative 0; Mismatches 15; Indels 5; Gaps 4;

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Qy      1149 GCTCCTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAA 1208
Db        10 GGTCCTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAA 69

Qy      1209 GGCCCTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTT 1268
Db        70 GGCCCTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTT 129

Qy      1269 GGCTGTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCA 1328
Db       130 GGCTGTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCA 189

Qy      1329 ATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGA 1388
Db       190 ATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGA 249

Qy      1389 GTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCG 1448
Db       250 GTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCG 309

Qy      1449 CCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCA 1508
Db       310 CCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCA 369

Qy      1509 GGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCG 1568
Db       370 GGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCG 429

Qy      1569 GCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTA 1628
Db       430 GCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTA 489

Qy      1629 CCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCT 1688
Db       490 CCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCT 549
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Qy       1689 GCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGG-CCCCCT 1747
              |||||||||||| |||||||||||||||||||||||||||||||||||||||| ||||||
Db        550 GCTCTCGGACAAAGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCCT 609

Qy       1748 GGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCT 1807
              |||||||||||||||||||||||| |||||||||||||||||||||| |||||||||
Db        610 GGAGCGACCTGCTTCTTTGGGCACTGGTGCTGAACAGGGCACAGATGGCCCTGTACTTCT 669

Qy       1808 GGGAGATGGGTTCCAAT-GCAGTTTCCTCAG-CTCTTGGGGCCTGTTTGCTG--CTCCGG 1863
              |||||||||| ||| || |||||||||||| |||||||||| | |||| |    ||||
Db        670 GGGAGATGGGGTCCCATGGCAGTTTCCTCAGCCTCTTGGGGCCCGGTTGCCGGCTCCCGG 729

Qy       1864 GTGATGGCACGCCTGGAGCC 1883
                ||||||||| || ||||||
Db        730 CGGATGGCACCCCCGGAGCC 749


RESULT 10
BQ723742
LOCUS       BQ723742                 883 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8241174 Lupski_sympathetic_trunk Homo sapiens cDNA clone
            IMAGE:6186968 5', mRNA sequence.
ACCESSION   BQ723742
VERSION     BQ723742.1  GI:21862639
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 883)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13580  row: d  column: 09
            High quality sequence stop: 557.
FEATURES             Location/Qualifiers
     source          1. .883
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6186968"
                     /sex="male"
                     /tissue_type="sympathetic trunk"
                     /dev_stage="adult, 16 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_sympathetic_trunk"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.9 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine); available through Life
                     Technologies."
ORIGIN

  Query Match             16.0%;  Score 651.6;  DB 5;  Length 883;
  Best Local Similarity   94.3%;  Pred. No. 5.8e-130;
  Matches  709;  Conservative    0;  Mismatches   39;  Indels    4;  Gaps    3;

Qy       2025 TGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGG 2084
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          1 TGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGG 60

Qy       2085 GGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTG 2144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTG 120

Qy       2145 GGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACCTTCAG 2204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACCTTCAG 180

Qy       2205 GAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAA 2264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAA 240

Qy       2265 TGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCG 2324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCG 300

Qy       2325 CCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCG 2384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCG 360

Qy       2385 CTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCT 2444
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCT 420

Qy       2445 GCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGG 2504
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCTGTTCTTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGG 480

Qy       2505 CTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCA 2564
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCA 540

Qy       2565 GGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTC 2624
              |||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db        541 GGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCAGGTCTGGCCATGCCTC 600

Qy       2625 A-CTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGG 2683
              | ||||||||||||||||||||||||||||||||||||||||||||    |||| |||| ||
Db        601 ACCTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACAGCGGCGA-CTAGAGG 659

Qy       2684 CTCTCACCTGCTTCCTCCTGGGC--GTGGGCTGCCGGCTGACCCCGGGTTTGTACCACCT 2741
              ||| |||||||||| |||||||||     |    |||  | |||||| | | || || |
Db        660 CTCCCACCTGCTTGCTCCTGGGCCGCGAGCTGCCCGCTTAACCCCGAGATCGTCCCCCTC 719

Qy       2742 GGGCCGCACTGTCCTCTGCATCGACTTCATGG 2773
              ||| | | |||  |||||||  ||  |   ||
Db        720 GGGACCCGCTGGGCTCTGCAAGGAAATTCGGG 751


RESULT 11
CA488844
LOCUS       CA488844                 864 bp    mRNA    linear   EST 14-NOV-2002
DEFINITION  AGENCOURT_10808212 MAPcL Homo sapiens cDNA clone IMAGE:6721042 5',
            mRNA sequence.
ACCESSION   CA488844
VERSION     CA488844.1  GI:24951635
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 864)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Kristi A. Egland, Ira Pastan
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
```

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          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM14281  row: i  column: 10
          High quality sequence stop: 571.
FEATURES             Location/Qualifiers
     source          1. .864
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6721042"
                     /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
                     hTERT-HME1, LNCaP"
                     /lab_host="EMDH10B"
                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification:  26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee  & Ira Pastan:  Discovery of new breast
                     cancer genes encoding  membrane and secreted proteins.
                     Manuscript submitted."
ORIGIN

  Query Match             15.9%;  Score 646.8;  DB 6;  Length 864;
  Best Local Similarity   94.4%;  Pred. No. 6.3e-129;
  Matches  668;  Conservative    0;  Mismatches   39;  Indels    1;  Gaps    1;

Qy       2966 GCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACG 3025
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACG 60

Qy       3026 TGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTG 3085
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTG 120

Qy       3086 GGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCG 3145
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCG 180

Qy       3146 TCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTT 3205
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTT 240

Qy       3206 ACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCC 3265
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCC 300

Qy       3266 TCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACT 3325
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACT 360

Qy       3326 TGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGG 3385
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGG 420

Qy       3386 CCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGG 3445
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGG 480

Qy       3446 AATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACT 3505
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACT 540

Qy       3506 CCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACA 3565
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACA 600

Qy       3566 TCCGCGAGTACGAACAGCGCCTGAAAGTGCT-GGAGCGGGAGGTCCAGCAGTGTAGCCGC 3624
             |||||||||||||||||||||| |||||| |||||||||||||||||||||  |||
Db        601 TCCGCGAGTACGAACAGCGCCTGANAGTGCTGGGAGCGGGAGGTCCAGCAGTGTACGCGC 660

Qy       3625 GTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCC 3672
                ||  |||                |       ||     |||
Db        661 TCCCCTGGGGGTTGNNNNNNNNNNNNNNCCNNNNNCNCCCCCNCCCCC 708


RESULT 12
BM982099/c
LOCUS       BM982099                655 bp    mRNA    linear   EST 21-FEB-2003
DEFINITION  UI-CF-EN1-acr-i-04-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
            UI-CF-EN1-acr-i-04-0-UI 3', mRNA sequence.
ACCESSION   BM982099
VERSION     BM982099.1  GI:19605256
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 655)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .655
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EN1-acr-i-04-0-UI"
                     /tissue_type="Primary Lung Cystic Fibrosis Epithelial
                     Cells"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EN1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EN1 is a normalized cDNA library containing the
                     following tissue(s): Primary Lung Cystic Fibrosis
                     Epithelial Cells. The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site.  Double stranded
                     cDNA was ligated to an EcoR I adaptor, digested with Not
                     I, and cloned directionally into pT7T3-Pac vector. The
                     oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CTGCTCAGGT.
                     TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
                     6hr to LPS 24h
                     TAG_LIB=UI-CF-EN1
                     TAG_SEQ=CTGCTCAGGT"
ORIGIN

  Query Match             15.8%;  Score 642.4;  DB 5;  Length 655;
  Best Local Similarity   99.8%;  Pred. No. 5.4e-128;
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  Matches  643;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3418 GAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCA 3477
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 GAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCA 595

Qy       3478 CGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTG 3537
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 CGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTG 535

Qy       3538 GACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTG 3597
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTG 475

Qy       3598 GAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGC 3657
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGC 415

Qy       3658 TCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGA 3717
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 TCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGA 355

Qy       3718 GCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGC 3777
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 GCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGC 295

Qy       3778 TCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCA 3837
             |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 TCATTTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCA 235

Qy       3838 TCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCG 3897
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCG 175

Qy       3898 GCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTTATC 3957
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTTATC 115

Qy       3958 CATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAG 4017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 CATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAG 55

Qy       4018 ATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAAAAAAA 4061
             |||||||||||||||||||||||||||||||||||||||||||||
Db          54 ATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAAAAAAA 11


RESULT 13
BF311909
LOCUS       BF311909               1090 bp    mRNA    linear   EST 21-NOV-2000
DEFINITION  601897749F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126764 5',
            mRNA sequence.
ACCESSION   BF311909
VERSION     BF311909.1  GI:11259680
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1090)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM1017  row: b  column: 13
            High quality sequence stop: 633.

FEATURES             Location/Qualifiers
     source          1. .1090
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4126764"
                     /tissue_type="neuroblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_19"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and  Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             15.7%;  Score 637.4;  DB 2;  Length 1090;
  Best Local Similarity   89.6%;  Pred. No. 7e-127;
  Matches  757;  Conservative    0;  Mismatches   71;  Indels   17;  Gaps    6;

Qy       1605 GGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCA 1664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCA 61

Qy       1665 GGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGA 1724
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Db         62 GGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGA 121

Qy       1725 TGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAG 1784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 TGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAG 181

Qy       1785 GGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGG 1844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGG 241

Qy       1845 GGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACG 1904
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Db        242 GGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACG 301

Qy       1905 GAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTA 1964
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTA 361

Qy       1965 TCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGA 2024
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Db        362 TCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGA 421

Qy       2025 TGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGG 2084
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Db        422 TGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGG 481

Qy       2085 GGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTG 2144
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Db        482 GGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTG 541

Qy       2145 GGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACCTTCAG 2204
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Db        542 GGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACCTTCAG 601

Qy       2205 GAAATCAGAAGAGGAGCCCACACGGGAGGAGCTA--GAGTTTGACATGGATA----GTGT 2258
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Db        602 GAAATCAGAAGAGGAG-CCACACGGGAGGAGCTAAGAGGTTTGACATGGACATAGGGTCA 660

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Db        661 TTACATGGGCGAAGGGGCTGTCCGGGACGGGGAGACCAAGCCGAGGAAGAAGCCGCTGGG 720

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Db        721 GGTCCCGCGGGCCAAACCGGGGCCGGCACGGGACGCATGGGGGGCCGAGCCAGGAGGGCG 780

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Db        781 CCCGGGGCCAAAGCCGGATGGGTCACATCTGAGGGGCGCACGTTGACCACCTCCGGGGCA 840

Qy       2429 ACGTG 2433
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RESULT 14
BG341728
LOCUS       BG341728                699 bp    mRNA    linear   EST 27-FEB-2001
DEFINITION  602463453F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576237 5',
            mRNA sequence.
ACCESSION   BG341728
VERSION     BG341728.1  GI:13148166
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 699)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1288  row: j  column: 14
            High quality sequence stop: 696.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4576237"
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                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           15.6%;  Score 635.2;  DB 4;  Length 699;
  Best Local Similarity   98.9%;  Pred. No. 2e-126;
  Matches  692;  Conservative    0;  Mismatches    3;  Indels    5;  Gaps    5;

Qy       3320 CCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCT 3379
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Qy       3380 CCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAA 3439
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Db         62 CCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAA 121

Qy       3440 CGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGA 3499
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Db        182 GCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGG 241

Qy       3560 GACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTA 3619
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Qy       3680 GGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGG 3739
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Db        362 GGCCG-CACCCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGG 420

Qy       3740 AGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGC 3799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGAAGCCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGC 480

Qy       3800 ACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCAC 3859
              |||||||||||||||||||||||||||||||||||||||||||||  ||  ||||||||||||||
Db        481 ACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTTGGGCACTGTCAGGACCAC 540

Qy       3860 C-TTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCC 3918
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3919 AGCCTGGGAGGATCAAGGCC-TGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTC 3977
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Db        601 AGCCTGGGAGGATCAAGGCCTTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTC 660

Qy       3978 CTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAG 4017
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Db        661 CTTGGGGTACCA-GGACCACAGA-CCCTCACCACTCACAG 698


RESULT 15
BI759746
LOCUS       BI759746                672 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603045620F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185949 5',
            mRNA sequence.
ACCESSION   BI759746
VERSION     BI759746.1  GI:15751324
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 672)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11464  row: g  column: 06
            High quality sequence stop: 668.
FEATURES             Location/Qualifiers
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/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 15.6%; Score 634.4; DB 4; Length 672;
Best Local Similarity 99.4%; Pred. No. 2.9e-126;
Matches 668; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

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Qy       2410 GTGACCATCTTCATGGGCAACGTGGTCA-GCTACCTGCTGTTCCTGCTGCTTTTCTCGCG 2468
             ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db          1 GTGACCATCTTCATGGGCAACGTGGTCACGCTACCTGCTGTTCCTGCTGCTTTTCTCGCG 60

Qy       2469 GGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTT 2528
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTT 120

Qy       2529 CTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAG 2588
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Db        121 CTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCA-GGCCTGAGCGGAGGCGGGGGCAG 179

Qy       2589 CCTCGCCAGCGGGGGCCCC-GGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCT 2647
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Db        180 CCTCGCCAGCGGGGGCCCCTGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCT 239

Qy       2648 ACCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCG 2707
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Db        300 TGGGCTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACT 359

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Qy       2828 AGATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCG 2887
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Db        540 TCCCAAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTC 599

Qy       3008 CCCAGGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCT 3067
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Db        600 CCCAGGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCT 659

Qy       3068 TCTGGGCACACC 3079
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Search completed: June 13, 2005, 08:20:49
Job time : 8327.65 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 18:12:43 ; Search time 439.26 Seconds
(without alignments)
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Title: US-09-869-486B-29
Perfect score: 4061
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Scoring table: IDENTITY_NUC
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1505	37.1	1524	3	US-09-030-607-109	Sequence 109, App
3	1505	37.1	1524	3	US-09-439-313-109	Sequence 109, App
4	1505	37.1	1524	3	US-09-352-616A-109	Sequence 109, App
5	1505	37.1	1524	3	US-09-232-149A-109	Sequence 109, App
6	1505	37.1	1524	4	US-09-159-812-109	Sequence 109, App
7	1505	37.1	1524	4	US-09-636-215-109	Sequence 109, App
8	1505	37.1	1524	4	US-09-685-166A-109	Sequence 109, App
9	1505	37.1	1524	4	US-09-115-453-109	Sequence 109, App
10	1505	37.1	1524	4	US-09-688-489-109	Sequence 109, App
11	1505	37.1	1524	4	US-09-679-426-109	Sequence 109, App
12	1505	37.1	1524	4	US-09-759-143-109	Sequence 109, App
13	1505	37.1	1524	4	US-09-651-236-109	Sequence 109, App
14	1230.2	30.3	1297	2	US-08-727-688-9	Sequence 9, Appli
15	815.8	20.1	3498	4	US-09-949-016-1003	Sequence 1003, Ap
16	814.2	20.0	3498	4	US-09-949-016-5521	Sequence 5521, Ap
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20	446.8	11.0	799	3	US-09-352-616A-8	Sequence 8, Appli
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24	446.8	11.0	799	4	US-09-685-166A-8	Sequence 8, Appli
25	446.8	11.0	799	4	US-09-115-453-8	Sequence 8, Appli
26	446.8	11.0	799	4	US-09-688-489-8	Sequence 8, Appli
27	446.8	11.0	799	4	US-09-679-426-8	Sequence 8, Appli
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c 37	395.8	9.7	801	3	US-09-232-149A-9	Sequence 9, Appli
c 38	395.8	9.7	801	4	US-09-159-812-9	Sequence 9, Appli
c 39	395.8	9.7	801	4	US-09-636-215-9	Sequence 9, Appli
c 40	395.8	9.7	801	4	US-09-685-166A-9	Sequence 9, Appli
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c 42	395.8	9.7	801	4	US-09-688-489-9	Sequence 9, Appli
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c 45	395.8	9.7	801	4	US-09-651-236-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-020-956-109
; Sequence 109, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1524 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-020-956-109

Query Match 37.1%; Score 1505; DB 3; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2557 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2616
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Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69
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Qy       2617 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2676
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2677 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2737 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2796
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2797 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2856
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2857 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2916
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       2917 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2976
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2977 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 3036
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       3037 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3096
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       3097 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3156
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3157 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3216
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Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3217 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3276
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Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3277 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3336
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3337 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3396
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Qy       3397 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3456
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3457 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3516
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Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3517 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3577 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3636
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3637 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3696
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3697 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 3756
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Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       3757 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 3816
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       3817 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 3876
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       3877 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 3936
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Qy       3997 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 4056
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Qy       4057 AAAAA 4061
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RESULT 2
US-09-030-607-109
; Sequence 109, Application US/09030607
; Patent No. 6262245
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Jiangchun
;    APPLICANT:  Dillon, Davin C.
;    TITLE OF INVENTION:  COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
;    NUMBER OF SEQUENCES:  224
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/030,607
;      FILING DATE:  25-FEB-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.427C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  109:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1524 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-09-030-607-109

  Query Match             37.1%;  Score 1505;  DB 3;  Length 1524;
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  Matches 1505;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2557 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2616
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Qy       2617 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2676
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Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2677 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2736
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Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2737 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2796
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Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2797 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2856
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2857 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2916
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Qy       2917 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2976
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Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2977 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 3036
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Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       3037 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3096
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       3097 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3156
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Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3157 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3216
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Qy       3217 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3276
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Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3277 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3336
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Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3337 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3396
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3397 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3456
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Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3457 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3516
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3517 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3577 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3636
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3637 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3696
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Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3697 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 3756
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       3757 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 3816
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       3817 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 3876
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       3877 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 3936
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       3937 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 3996
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       3997 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 4056
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Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 1509

Qy       4057 AAAAA 4061
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Db       1510 AAAAA 1514
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RESULT 3
US-09-439-313-109
; Sequence 109, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan Louise
;  APPLICANT:  Jiang Yuqui
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Kalos, Michael
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Retter, Mark
;  APPLICANT:  Solk, John
;  APPLICANT:  Day, Craig
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C9
;  CURRENT APPLICATION NUMBER: US/09/439,313
;  CURRENT FILING DATE:  1999-11-12
;  NUMBER OF SEQ ID NOS: 575
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-439-313-109

  Query Match            37.1%;  Score 1505;  DB 3;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1505;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2557 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2616
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Qy      2677 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2736
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Qy      2737 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2796
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Qy      2797 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2856
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Qy      2857 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2916
Db       310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy      2917 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2976
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Qy      2977 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 3036
Db       430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy      3037 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3096
Db       490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy      3097 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3156
Db       550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy      3157 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3216
Db       610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy      3217 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3276
Db       670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy      3277 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3336
Db       730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy      3337 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3396
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Qy      3397 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3456
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Qy      3457 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3516
Db       910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy      3517 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
Db       970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy      3577 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3636
Db      1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

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Db      1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy      3697 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 3756
Db      1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy      3757 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 3816
Db      1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy      3817 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 3876
Db      1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy      3877 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 3936
Db      1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy      3937 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 3996
Db      1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy      3997 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 4056
Db      1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 1509

Qy      4057 AAAAA 4061
Db      1510 AAAAA 1514
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RESULT 4
US-09-352-616A-109
; Sequence 109, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Harlocker, Susan Louise
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Mitcham, Jennifer Lynn
;  TITLE OF INVENTION:  COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
;  TITLE OF INVENTION:  OF PROSTATE CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE:  210121.427C8
;  CURRENT APPLICATION NUMBER: US/09/352,616A
;  CURRENT FILING DATE:  1999-07-13
;  NUMBER OF SEQ ID NOS:  472
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-352-616A-109

  Query Match             37.1%;  Score 1505;  DB 3;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1505;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2557 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2616
Db        10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy      2617 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2676
Db        70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy      2677 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2736
Db       130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy      2737 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2796
Db       190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy      2797 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2856
Db       250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309
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Qy       2857 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2916
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Qy       2917 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2976
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Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2977 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 3036
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Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3157 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3216
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Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3277 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3336
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Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

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Qy       3397 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3456
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Qy       3457 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3516
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Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3517 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
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Qy       3577 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3636
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Qy       3697 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 3756
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Qy       3757 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 3816
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Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 1509

Qy       4057 AAAAA 4061
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RESULT 5
US-09-232-149A-109
; Sequence 109, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-109

Query Match 37.1%; Score 1505; DB 3; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2557 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2616
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Qy       3037 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3096
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Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3157 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3216
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Qy       3277 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3336
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Qy       3517 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
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Qy       3637 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3696
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Qy       3697 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 3756
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Qy       3817 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 3876
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Qy       3877 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 3936
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Db       1510 AAAAA 1514
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RESULT 6
US-09-159-812-109
; Sequence 109, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-159-812-109

Query Match 37.1%; Score 1505; DB 4; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2557 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2616
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Qy       2737 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2796
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Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       3097 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3156
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Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3157 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3216
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Qy       3217 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3276
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Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3277 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3336
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Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789
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Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3397 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3456
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Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

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Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3517 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
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Qy       3577 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3636
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Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3697 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 3756
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Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       3757 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 3816
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       3817 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 3876
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       3877 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 3936
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       3937 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 3996
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       3997 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 4056
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 1509

Qy       4057 AAAAA 4061
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Db       1510 AAAAA 1514
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RESULT 7
US-09-636-215-109
; Sequence 109, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Panger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.42717C17
;  CURRENT APPLICATION NUMBER: US/09/636,215
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS:  852
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-636-215-109

  Query Match             37.1%;  Score 1505;  DB 4;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1505;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2557 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2616
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy       2617 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2676
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2677 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2737 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2796
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2797 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2856
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2857 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2916
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       2917 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2976
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2977 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 3036
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Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       3037 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3096
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       3097 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3156
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3157 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3216
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3217 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3276
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Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3277 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3336
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3337 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3396
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3397 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3457 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3516
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3517 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3577 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3636
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3637 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3696
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3697 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 3756
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       3757 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 3816
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       3817 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 3876
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       3877 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 3936
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       3937 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 3996
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Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       3997 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 4056
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Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 1509

Qy       4057 AAAAA 4061
              |||||
Db       1510 AAAAA 1514


RESULT 8
US-09-685-166A-109
; Sequence 109, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C21
;  CURRENT APPLICATION NUMBER: US/09/685,166A
;  CURRENT FILING DATE:  2000-10-10
;  NUMBER OF SEQ ID NOS: 898
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-685-166A-109

  Query Match             37.1%;  Score 1505;  DB 4;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1505;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2557 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2616
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy       2617 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2676
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Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2677 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2736
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Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2737 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2796
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2797 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2856
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2857 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2916
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Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       2917 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2976
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Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2977 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 3036
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Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       3037 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3096
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

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Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3157 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3216
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Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3217 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3276
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Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3277 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3336
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Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3337 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3396
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Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849
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Qy       3397 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3456
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Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3457 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3516
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Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3517 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3577 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3636
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3637 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3696
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3697 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 3756
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       3757 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 3816
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Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       3817 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 3876
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       3877 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 3936
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       3937 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 3996
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       3997 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 4056
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Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 1509

Qy       4057 AAAAA 4061
             |||||
Db       1510 AAAAA 1514


RESULT 9
US-09-115-453-109
; Sequence 109, Application US/09115453B
; Patent No. 6657056
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT: Dillon, Davin C.
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
;  TITLE OF INVENTION: METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.427C4
;  CURRENT APPLICATION NUMBER: US/09/115,453B
;  CURRENT FILING DATE: 1998-07-14
;  NUMBER OF SEQ ID NOS: 228
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-115-453-109

  Query Match            37.1%;  Score 1505;  DB 4;  Length 1524;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1505;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2557 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2616
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy       2617 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2676
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Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2677 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2737 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2796
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Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2797 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2856
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Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2857 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2916
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Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       2917 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2976
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2977 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 3036
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       3037 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3096
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       3097 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3156
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3157 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3216
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3217 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3276
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3277 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3336
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3337 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3396
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3397 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3456
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3457 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3516
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3517 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3577 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3636
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Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3637 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3696
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Qy         3697 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 3756
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Qy         3757 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 3816
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Db         1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

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Qy         3877 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 3936
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy         3997 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 4056
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 1509

Qy         4057 AAAAA 4061
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Db         1510 AAAAA 1514
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RESULT 10
US-09-688-489-109
; Sequence 109, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-688-489-109

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  Query Match             37.1%;  Score 1505;  DB 4;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1505;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         2617 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2676
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Db          190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy         2797 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2856
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Qy         2977 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 3036
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Db          430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy         3037 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3096
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Db          490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

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Db          550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy         3157 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3216
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Qy         3217 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3276
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Db          670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy         3277 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3336
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Db          850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy         3457 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3516
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Db          910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy         3517 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy         3577 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3636
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy         3637 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3696
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Db         1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy         3697 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 3756
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Db         1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy         3757 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 3816
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Db         1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy         3817 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 3876
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Db         1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy         3877 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 3936
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Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 1509

Qy       4057 AAAAA 4061
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Db       1510 AAAAA 1514


RESULT 11
US-09-679-426-109
; Sequence 109, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C20
;  CURRENT APPLICATION NUMBER: US/09/679,426
;  CURRENT FILING DATE:  2000-10-02
;  NUMBER OF SEQ ID NOS:  895
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-679-426-109

  Query Match             37.1%;  Score 1505;  DB 4;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1505;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy       2617 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2676
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Qy       2857 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2916
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Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       3037 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3096
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Qy       3097 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3156
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Qy       3157 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3216
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Qy       3217 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3276
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Qy       3277 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3336
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Qy       3337 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3396
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Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3397 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3456
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Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

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Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3517 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
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Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3577 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3636
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Qy       3637 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3696
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

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Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       3757 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 3816
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Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       3817 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 3876
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Qy       3877 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 3936
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Qy       3937 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 3996
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Qy       3997 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 4056
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Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 1509

Qy       4057 AAAAA 4061
             |||||
Db       1510 AAAAA 1514


RESULT 12
US-09-759-143-109
; Sequence 109, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C23
;  CURRENT APPLICATION NUMBER: US/09/759,143
;  CURRENT FILING DATE:  2001-01-12
;  NUMBER OF SEQ ID NOS:  934
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-759-143-109

  Query Match             37.1%;  Score 1505;  DB 4;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1505;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2557 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2616
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy       2617 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2676
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Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2677 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2736
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Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2737 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2796
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2797 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2856
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Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2857 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2916
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       2917 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2976
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Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2977 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 3036
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Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       3037 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3096
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Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       3097 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3156
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3157 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3216
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Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3217 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3276
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3277 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3336
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3337 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3396
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3397 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3456
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Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3457 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3516
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Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3517 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
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Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3577 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3636
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3637 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3696
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3697 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 3756
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Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       3757 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 3816
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Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       3817 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 3876
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Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       3877 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 3936
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Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       3937 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 3996
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Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449

Qy       3997 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 4056
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Db       1450 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 1509

Qy       4057 AAAAA 4061
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Db       1510 AAAAA 1514


RESULT 13
US-09-651-236-109
; Sequence 109, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.42718C18
;  CURRENT APPLICATION NUMBER: US/09/651,236
;  CURRENT FILING DATE:  2000-08-29
;  NUMBER OF SEQ ID NOS:  865
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-651-236-109

  Query Match             37.1%;  Score 1505;  DB 4;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1505;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2557 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2616
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2617 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2676
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Qy       2677 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2736
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2737 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2796
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Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2797 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2856
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2857 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2916
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Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       2917 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2976
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Qy       2977 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 3036
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Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       3037 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3096
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Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

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Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3157 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3216
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Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3277 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3336
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Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3337 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3396
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Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

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Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3457 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3516
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Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3517 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
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Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3577 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3636
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3637 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3696
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Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3697 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 3756
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Db       1150 CTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCACAGGGG 1209

Qy       3757 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 3816
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCC 1269

Qy       3817 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 3876
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Db       1270 TTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGACCACCTTTGGGAGTGTCATCC 1329

Qy       3877 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 3936
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Db       1330 TTACAAACCACAGCATGCCCGGCTCCTCCCAGAACCAGTCCCAGCCTGGGAGGATCAAGG 1389

Qy       3937 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 3996
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Db       1390 CCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCCTTGGGGTAACAGGGACCA 1449
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Qy       3997 CAGACCCCTCACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAAA 4056
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Qy       4057 AAAAA 4061
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Db       1510 AAAAA 1514
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RESULT 14
US-08-727-688-9
; Sequence 9, Application US/08727688
; Patent No. 5919638
; GENERAL INFORMATION:
; APPLICANT: Russell, John C.
; TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road D377/AP6D
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,688
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5967.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 937-0378
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-727-688-9

Query Match 30.3%; Score 1230.2; DB 2; Length 1297;
Best Local Similarity 98.5%; Pred. No. 8e-281;
Matches 1279; Conservative 0; Mismatches 16; Indels 4; Gaps 4;

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Qy       2558 TGCGCCAGGGCCTGAGCGGA-GGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2616
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Db          1 TGCGCNGGAGCCTGAGCGGAGGGTGTGCGCAGCCTCGCCAGCGGGGGCCCCGGGCTGNGC 60

Qy       2617 CA-TGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGA 2675
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Db         61 CATTGCCTCACTGAGCCAGCGCCTGC-CTNCTACCTCGCCGACAGCTGGAACCAGTGCGA 119

Qy       2676 CCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTA 2735
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Db        120 CCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTA 179

Qy       2736 CCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCA 2795
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Db        180 CCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCA 239

Qy       2796 CATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAA 2855
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Db        240 CATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAA 299

Qy       2856 GGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCAC 2915
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCAC 359

Qy       2916 GGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTA 2975
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Db        360 GGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTA 419

Qy       2976 CCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCAT 3035
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 CCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCAT 479

Qy       3036 GGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGC 3095
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 GGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGC 539

Qy       3096 GGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCT 3155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCT 599

Qy       3156 GCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGG 3215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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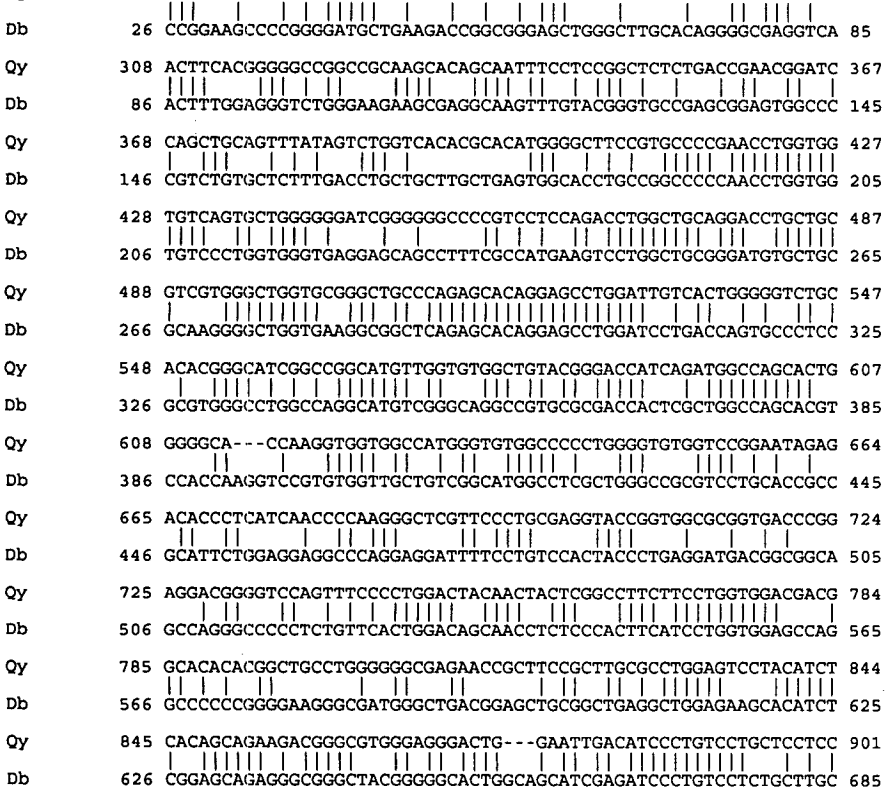
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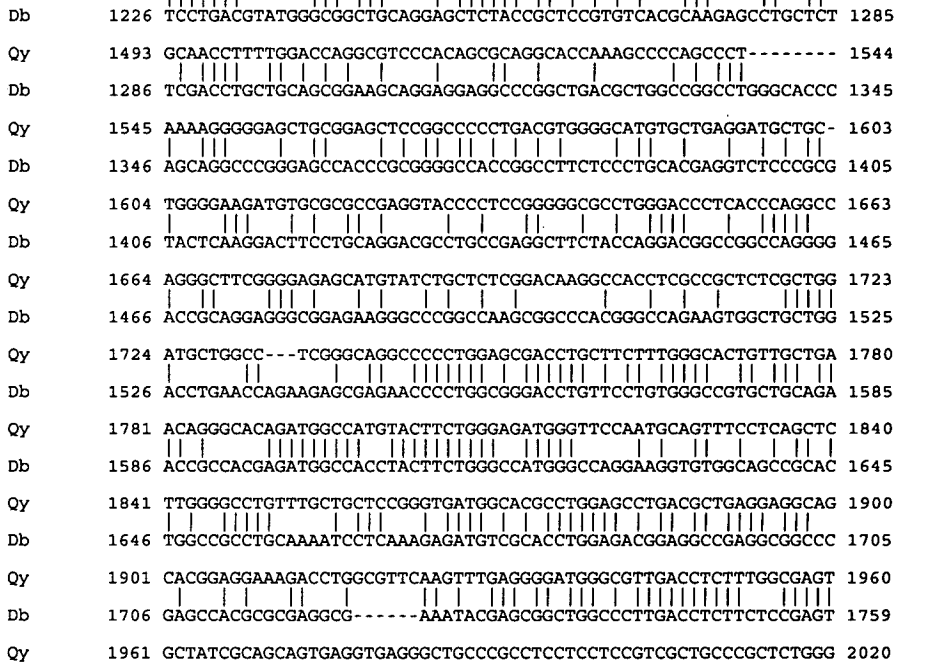
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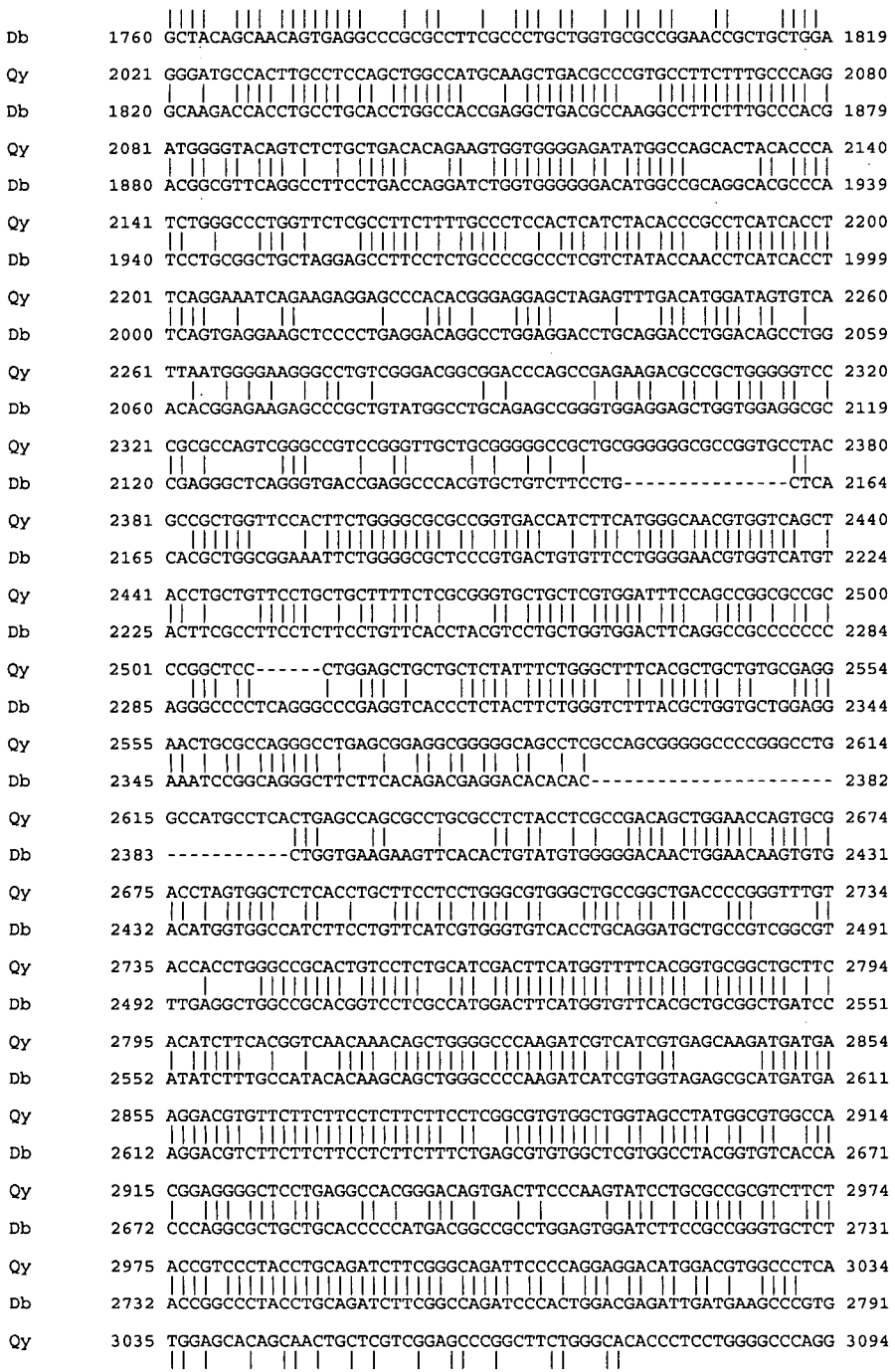
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RESULT 15
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; Sequence 1003, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1003
; LENGTH: 3498
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1003

Query Match 20.1%; Score 815.8; DB 4; Length 3498;
Best Local Similarity 55.6%; Pred. No. 1.2e-182;
Matches 1916; Conservative 0; Mismatches 1407; Indels 126; Gaps 13;







Search completed: June 13, 2005, 08:38:56
Job time : 445.26 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 06:26:36 ; Search time 10260.1 Seconds
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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ACCESSION AY297045
VERSION AY297045.1 GI:31335332
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3879)
AUTHORS Hofmann,T., Chubanov,V., Gudermann,T. and Montell,C.
TITLE TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent Selective Cation Channel
JOURNAL Curr. Biol. 13 (13), 1153-1158 (2003)
MEDLINE 22726392
PUBMED 12842017
REFERENCE 2 (bases 1 to 3879)
AUTHORS Chubanov,V., Hofmann,T., Gudermann,T. and Montell,C.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-2003) Institut fuer Pharmakologie und Toxikologie, Philipps-Universitaet Marburg, Karl-von-Frisch-Strasse 1, Marburg D-35033, Germany
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ORIGIN

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RESULT 2
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DEFINITION Homo sapiens mRNA for transient receptor potential ion channel melastatin subgroup member 4 protein (TRPM4 gene).
ACCESSION AJ575813
VERSION AJ575813.1 GI:32487283
KEYWORDS transient receptor potential ion channel melastatin subgroup member 4 protein; TRPM4 gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nilius,B., Prenen,J., Droogmans,G., Voets,T., Vennekens,R., Freichel,M., Wissenbach,U. and Flockerzi,V.
TITLE Voltage Dependence of the Ca2+-activated Cation Channel TRPM4
JOURNAL J. Biol. Chem. 278 (33), 30813-30820 (2003)

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  MEDLINE   22791733
   PUBMED   12799367
REFERENCE   2  (bases 1 to 4042)
  AUTHORS   Wissenbach,U.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUL-2003) Wissenbach U., University of the Saarland,
            Institue for Pharmacology and Toxicology, 66421 Homburg - Saar,
            Saarland, GERMANY
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ORIGIN

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RESULT 3
BD270156
LOCUS       BD270156                4061 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Characterization of a calcium channel family.
ACCESSION   BD270156
VERSION     BD270156.1  GI:33079924
KEYWORDS    JP 2002536966-A/15.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4061)
  AUTHORS   Scharenberg,A.M.
  TITLE     Characterization of a calcium channel family
  JOURNAL   Patent: JP 2002536966-A 15 05-NOV-2002;
            BETH ISRAEL DEACONESS MEDICAL CENTER INC
COMMENT     OS   Homo sapiens (human)
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            PD   05-NOV-2002
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            PR   30-DEC-1998 US    60/114220,29-JAN-1999 US    60/120018 PR
            22-JUN-1999 US    60/140415
            PI   ANDREW M SCHARENBERG
            PC   C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K35/76,A61K38/
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ORIGIN

  Query Match             100.0%;  Score 3642;  DB 6;  Length 4061;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3642;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         73 ATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAGAAGAAGACCTGC 132

Qy         61 ACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAGTGTGGGCGCCCC 120
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Qy      1381 GCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCG 1440
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Db      3193 GCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCG 3252

Qy      3181 CAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATC 3240
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RESULT 4
AF497623
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DEFINITION  Homo sapiens cation channel TRPM4B (TRPM4B) mRNA, complete cds.
ACCESSION   AF497623
VERSION     AF497623.1  GI:20269878
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 4061)
  AUTHORS   Launay,P., Fleig,A., Perraud,A.L., Scharenberg,A.M., Penner,R. and
            Kinet,J.P.
  TITLE     TRPM4 is a Ca2+-activated nonselective cation channel mediating
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  JOURNAL   Cell 109 (3), 397-407 (2002)
  MEDLINE   22011788
   PUBMED   12015988
REFERENCE   2  (bases 1 to 4061)
  AUTHORS   Perraud,A.-L. and Scharenberg,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-APR-2002) Pediatrics, Washington, 1959 NE Pacific
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ORIGIN

  Query Match           100.0%;  Score 3642;  DB 9;  Length 4061;
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Qy        421 GGGCTGGTGCCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACG 480
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Qy        661 GTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACAC 720
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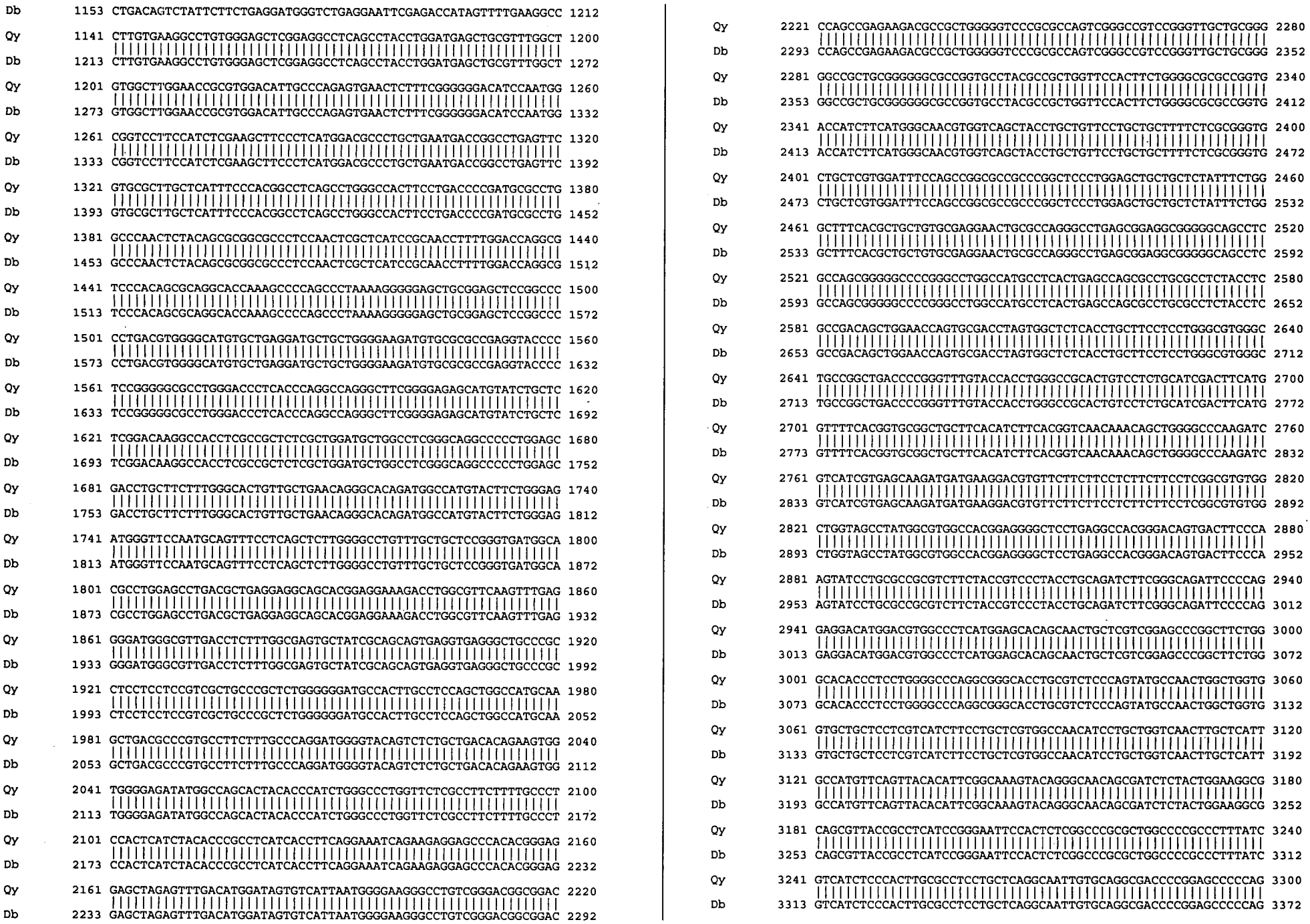
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RESULT 5
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DEFINITION  Sequence 9 from Patent WO0210382.
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VERSION     AX443227.1  GI:21690622
KEYWORDS    .
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wissenbach,U.
  TITLE     Trp8, trp9 and trp10, markers for cancer
  JOURNAL   Patent: WO 0210382-A 9 07-FEB-2002;
            Wissenbach, Ulrich (DE)
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ORIGIN

  Query Match           100.0%;  Score 3640.4;  DB 6;  Length 4042;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3641;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAGAAGAAGACCTGC 60
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Qy         61 ACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAGTGTGGGCGCCCC 120
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Qy        121 CGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCCGTGGTGACCGTG 180
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Qy        181 TGGGACAGCGATGCACACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTC 240
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Qy        721 GGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAG 780
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Qy        781 AAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGT 840
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Db        822 AAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGT 881

Qy        841 GATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTC 900
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Qy        901 GTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCC 960
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Qy        961 CCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCC 1020
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Qy    1021 AAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTC 1080
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Qy    1081 CTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCC 1140
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Qy    1141 CTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCT 1200
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Qy    1201 GTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGG 1260
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Db    1242 GTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGG 1301

Qy    1261 CGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTC 1320
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Qy    1321 GTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTG 1380
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Qy    1381 GCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCG 1440
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Qy    1441 TCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCC 1500
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Qy    1621 TCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGC 1680
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Qy    1681 GACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAG 1740
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Db    1722 GACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAG 1781

Qy    1741 ATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCA 1800
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Db    1782 ATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCA 1841

Qy    1801 CGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAG 1860
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Qy    1861 GGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGC 1920
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Qy    1921 CTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAA 1980
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Qy    2041 TGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCT 2100
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Qy    2101 CCACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAG 2160
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Db    2142 CCACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAG 2201

Qy    2161 GAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGAC 2220
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Qy    2401 CTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGG 2460
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Qy    2461 GCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTC 2520
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Qy    2581 GCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGC 2640
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Qy       3481 CAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAG 3540

Db       3522 CAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAG 3581

Qy       3541 CAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCC 3600

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DEFINITION  Homo sapiens cDNA FLJ20041 fis, clone COL00423.
ACCESSION   AK000048
VERSION     AK000048.1  GI:7019878
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
            Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
            Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3810)
  AUTHORS   Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
            Shibahara,T., Tanaka,T. and Nakamura,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,
            University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1,
            Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp,
            Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            International Trade and Industry of Japan; cDNA full insert
            sequencing: Research Association for Biotechnology; cDNA library
            construction, 5'- & 3'-end one pass sequencing: Departent of
            Virology and Human Genome Center, Institute of Medical Science,
            University of Tokyo (partly supported by Science and Technology
            Agency).
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ORIGIN
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Db        181 GCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCC 240

Qy        440 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 499

Db        241 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 300

Qy        500 GTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGG 559

Db        301 GTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGG 360

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Db        361 GTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGT 420

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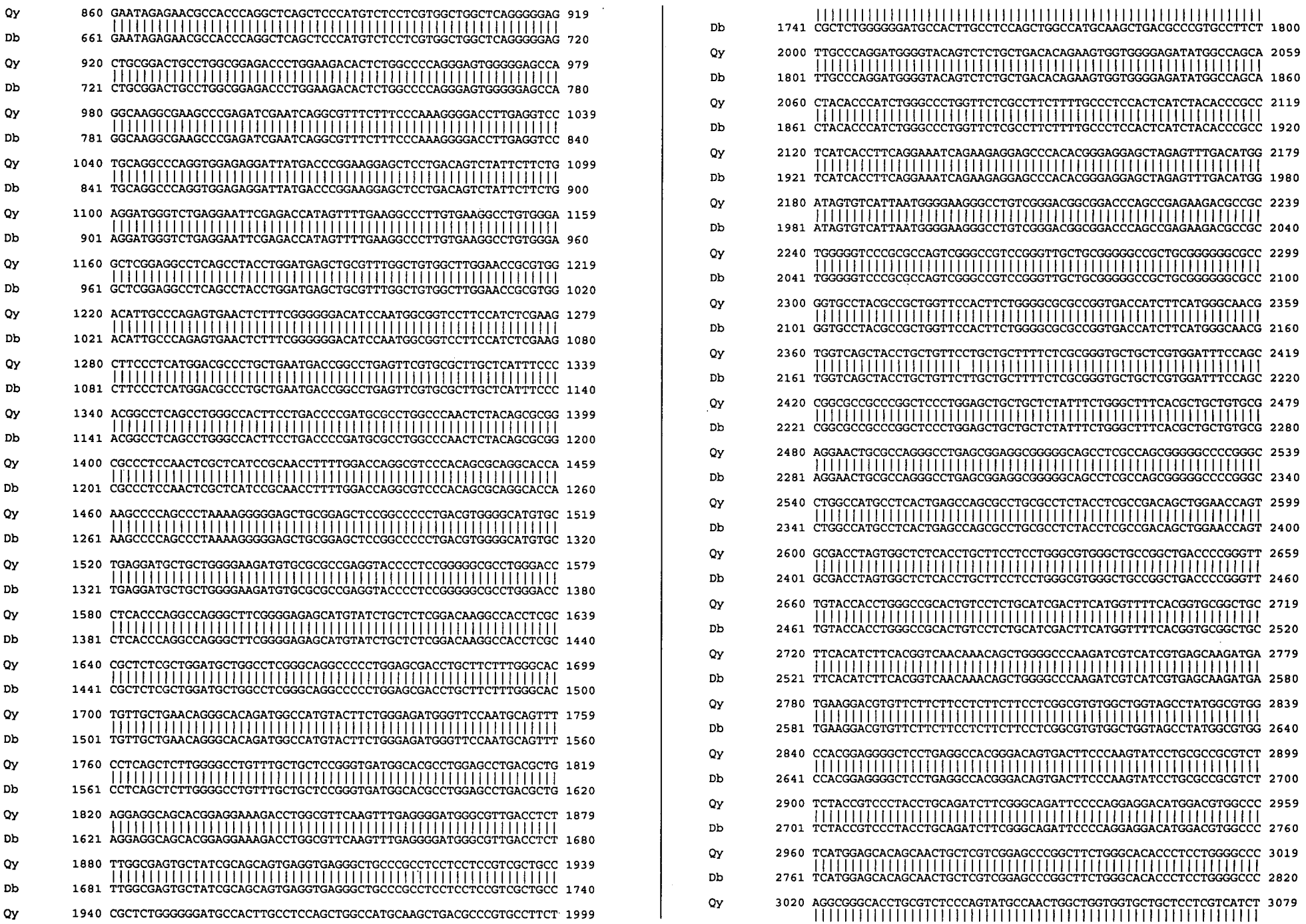
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RESULT 7
AX235183
LOCUS       AX235183               3900 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 1 from Patent WO0162794.
ACCESSION   AX235183
VERSION     AX235183.1  GI:15593774
KEYWORDS    .
SOURCE      Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Glucksmann,M.A., Curtis,R.A. and Lora,J.M.
  TITLE     18607, a human calcium channel
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            Millennium Pharmaceuticals, Inc. (US)
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ORIGIN

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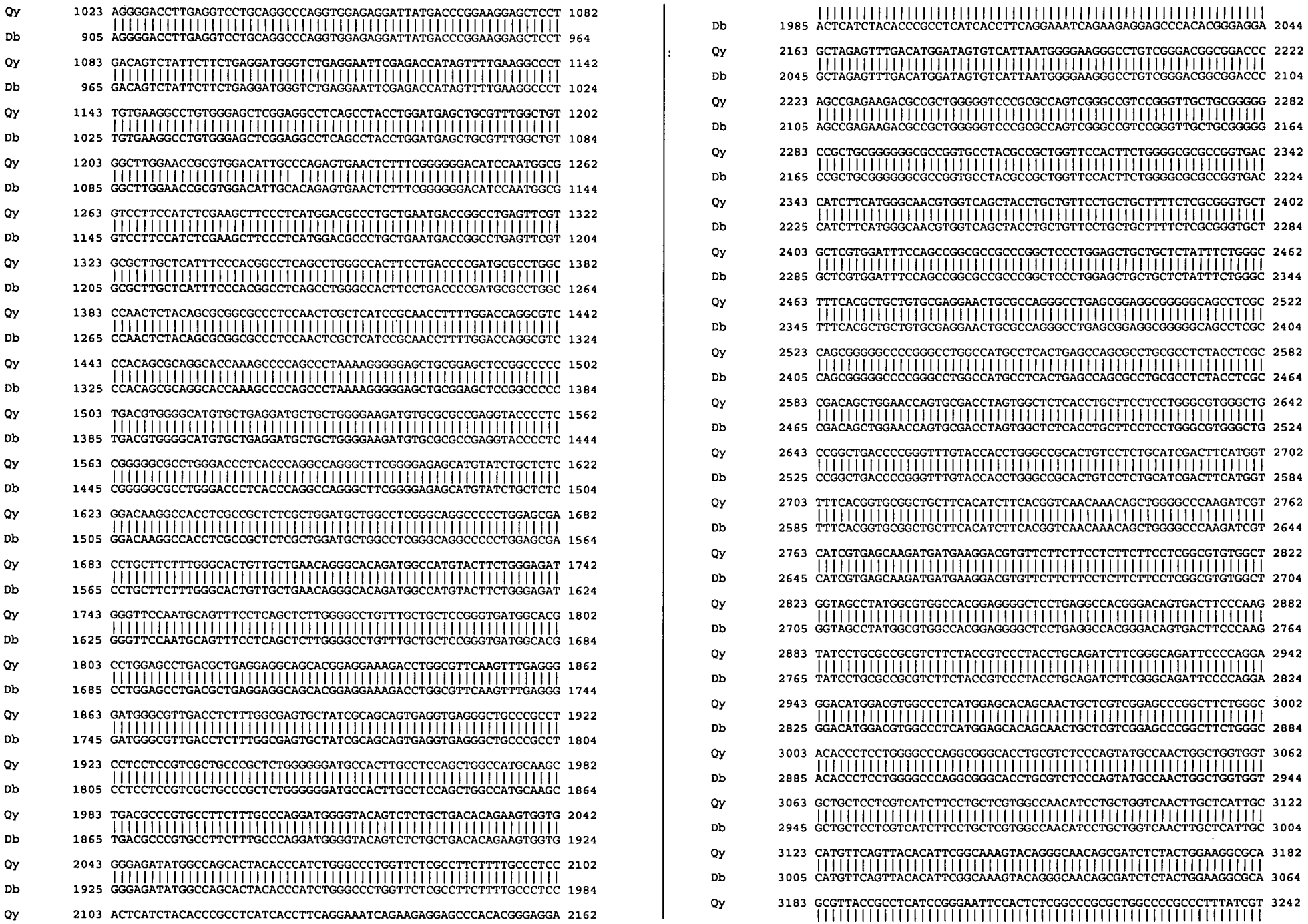
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RESULT 8
AX235185
LOCUS       AX235185               3387 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 3 from Patent WO0162794.
ACCESSION   AX235185
VERSION     AX235185.1  GI:15593776
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Glucksmann,M.A., Curtis,R.A. and Lora,J.M.
  TITLE     18607, a human calcium channel
  JOURNAL   Patent: WO 0162794-A 3 30-AUG-2001;
            Millennium Pharmaceuticals, Inc. (US)
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ORIGIN

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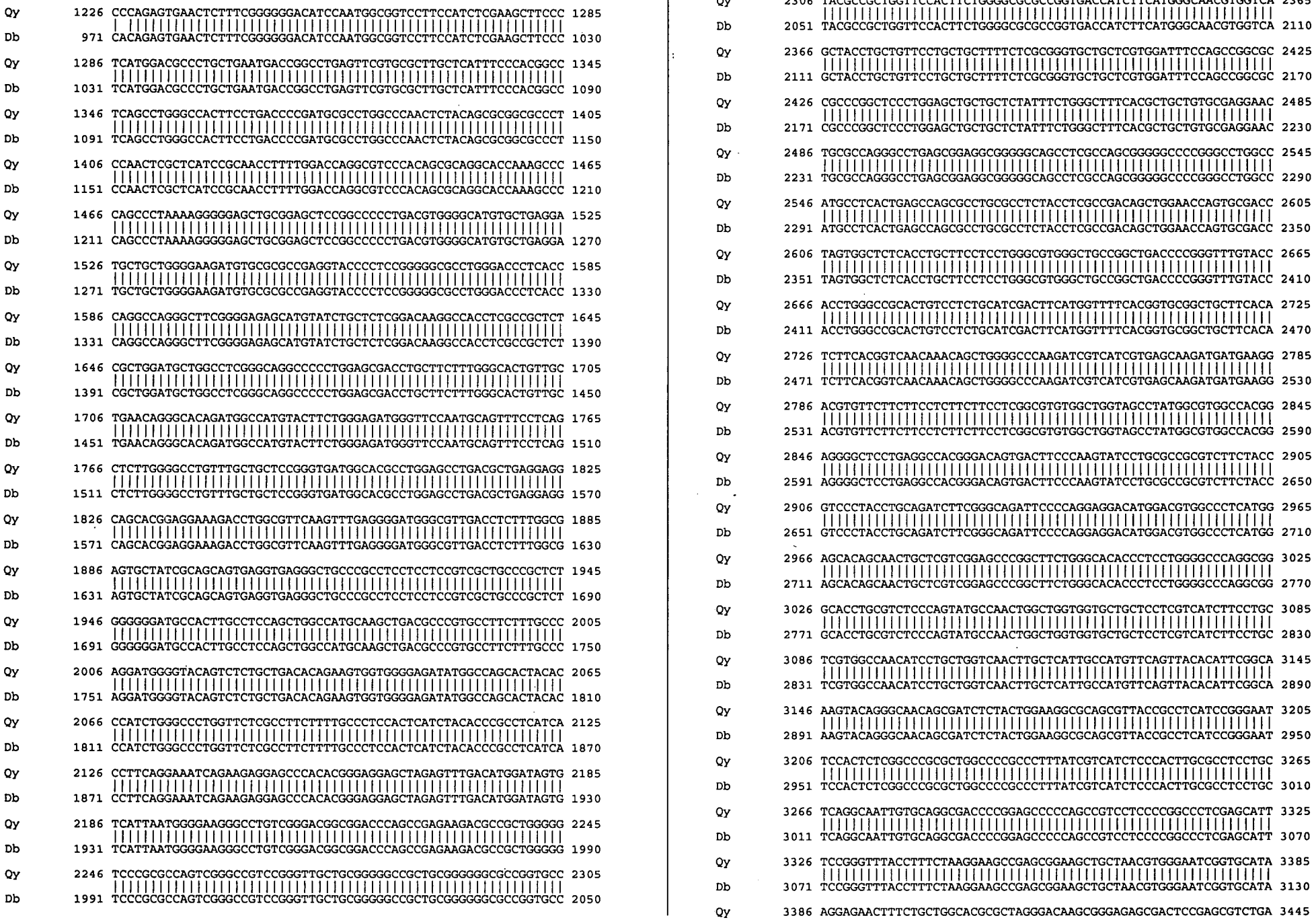
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RESULT 9
CQ715325
LOCUS       CQ715325                3402 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 1259 from Patent WO02068579.
ACCESSION   CQ715325
VERSION     CQ715325.1  GI:42276182
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 1259 06-SEP-2002;
            PE Corporation (NY) (US)
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ORIGIN

  Query Match             91.5%;  Score 3333;  DB 6;  Length 3402;
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REFERENCE   1
  AUTHORS   Hillman,J.L., Tang,Y.T., Yue,H., Elliott,V.S., Tribouley,C.M.,
            Lee,E.A., Ramkumar,J., Lal,P., Xu,Y., Warren,B.A., Hafalia,A.J.,
            Baughn,M.R., Azimzai,Y., Batra,S., Burford,N., Yao,M.G.,
            Nguyen,D.B., Lu,D.A., Walia,N.K., Au-Young,J. and Patterson,C.
  JOURNAL   Patent: WO 0198353-A 88 27-DEC-2001;
            Incyte Genomics, Inc. (US)
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ORIGIN

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ACCESSION   AY297044
VERSION     AY297044.1  GI:31335330
KEYWORDS    .
SOURCE      Homo sapiens (human)
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REFERENCE   1  (bases 1 to 3523)
  AUTHORS   Hofmann,T., Chubanov,V., Gudermann,T. and Montell,C.
  TITLE     TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent
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  JOURNAL   Curr. Biol. 13 (13), 1153-1158 (2003)
  MEDLINE   22726392
   PUBMED   12842017
REFERENCE   2  (bases 1 to 3523)
  AUTHORS   Chubanov,V., Gudermann,T., Hofmann,T. and Montell,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAY-2003) Institut fuer Pharmakologie und
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ORIGIN

Query Match 87.9%; Score 3199.8; DB 9; Length 3523;
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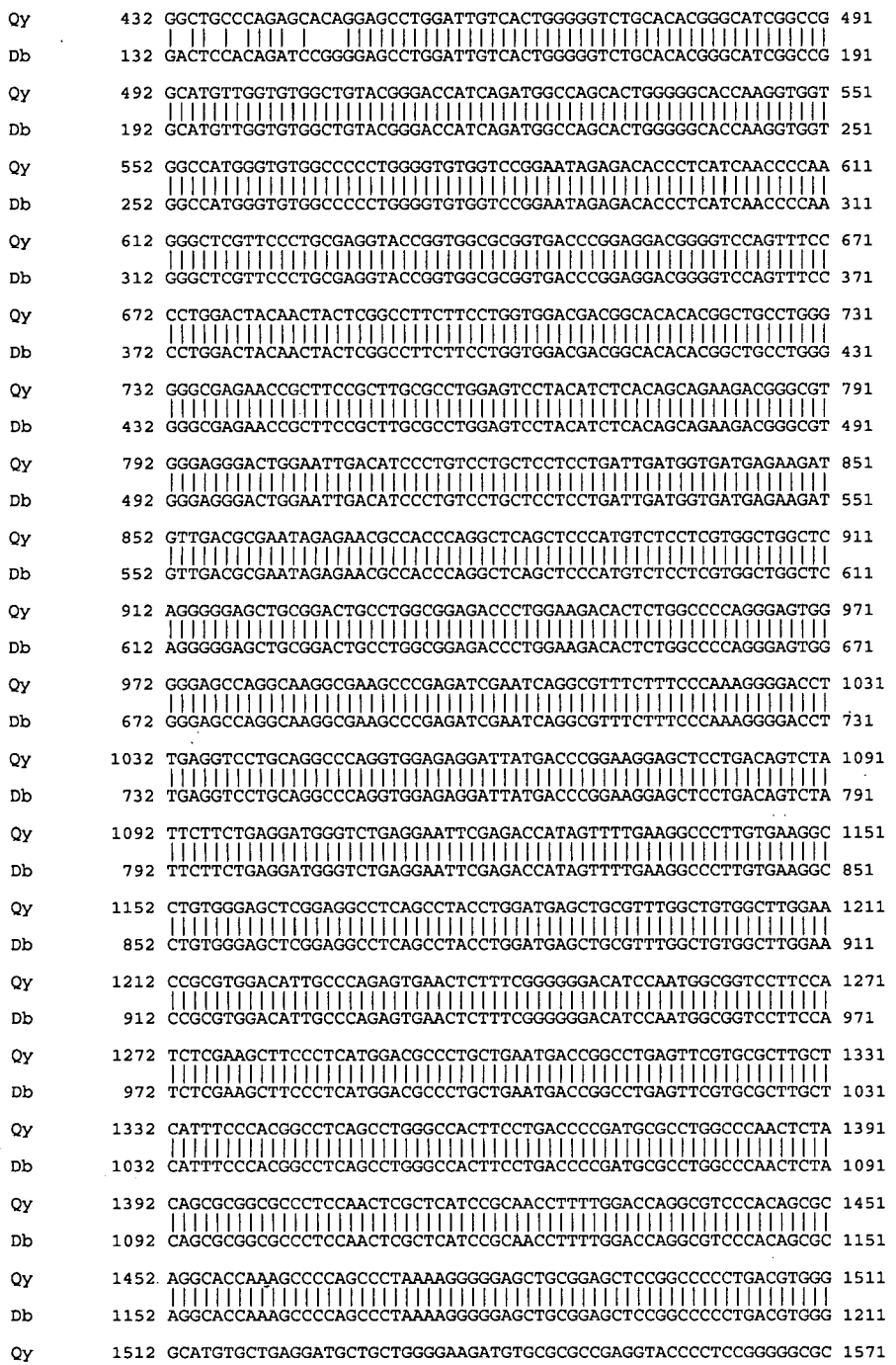
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VERSION AY046396.1 GI:15617228
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REFERENCE 1 (bases 1 to 3701)
AUTHORS Xu,X.Z., Moebius,F., Gill,D.L. and Montell,C.
TITLE Regulation of melastatin, a TRP-related protein, through interaction with a cytoplasmic isoform
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (19), 10692-10697 (2001)
MEDLINE 21438010
PUBMED 11535825
REFERENCE 2 (bases 1 to 3701)
AUTHORS Xu,X.-Z., Moebius,F., Gill,D.L. and Montell,C.
TITLE Direct Submission
JOURNAL Submitted (17-JUL-2001) Biological Chemistry, Johns Hopkins Univ School of Medicine, 725 N. Wolfe Street, Baltimore, MD 21205, USA
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ORIGIN

Query Match 87.8%; Score 3196.6; DB 9; Length 3701;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3202; Conservative 0; Mismatches 9; Indels 0; Gaps 0;


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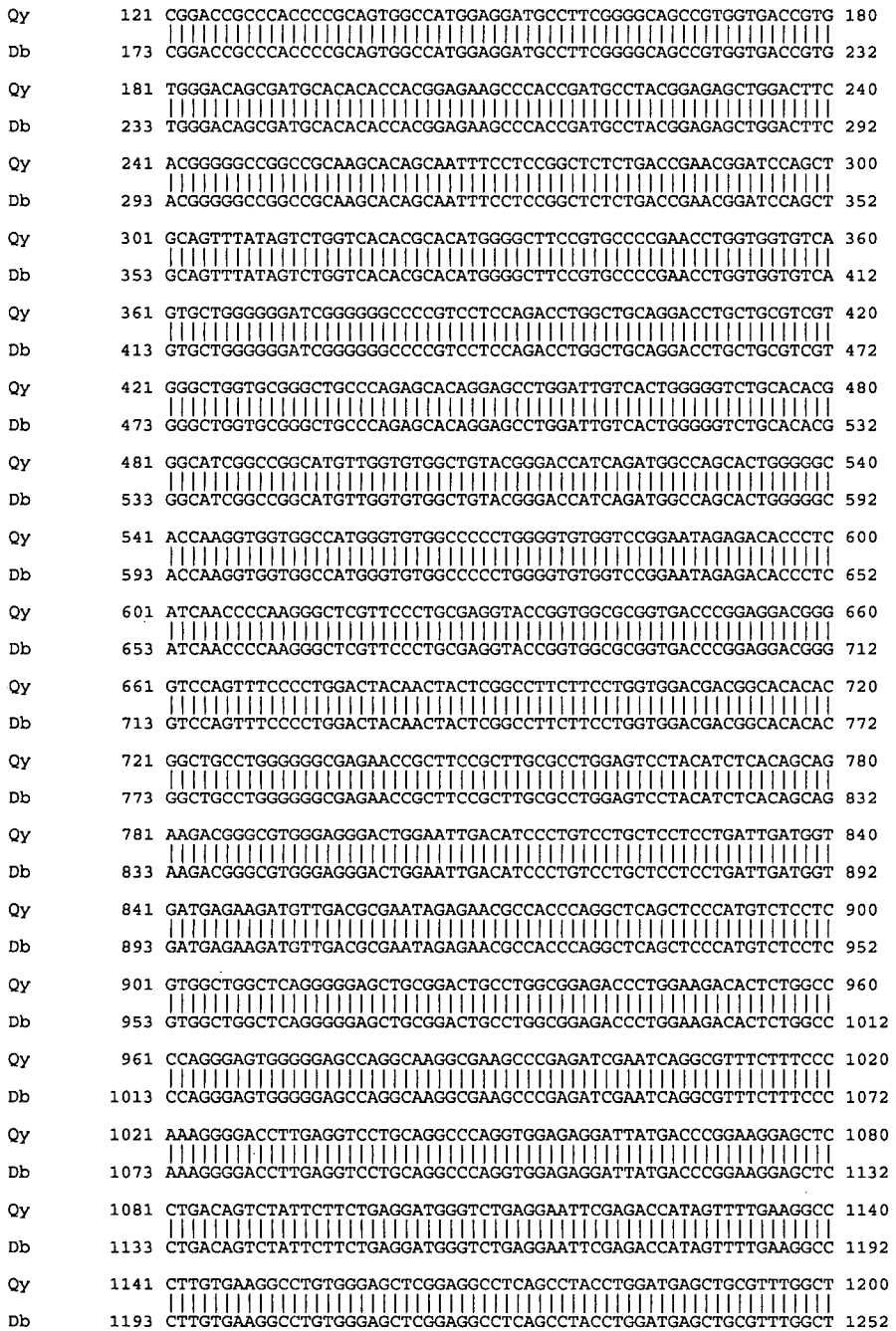
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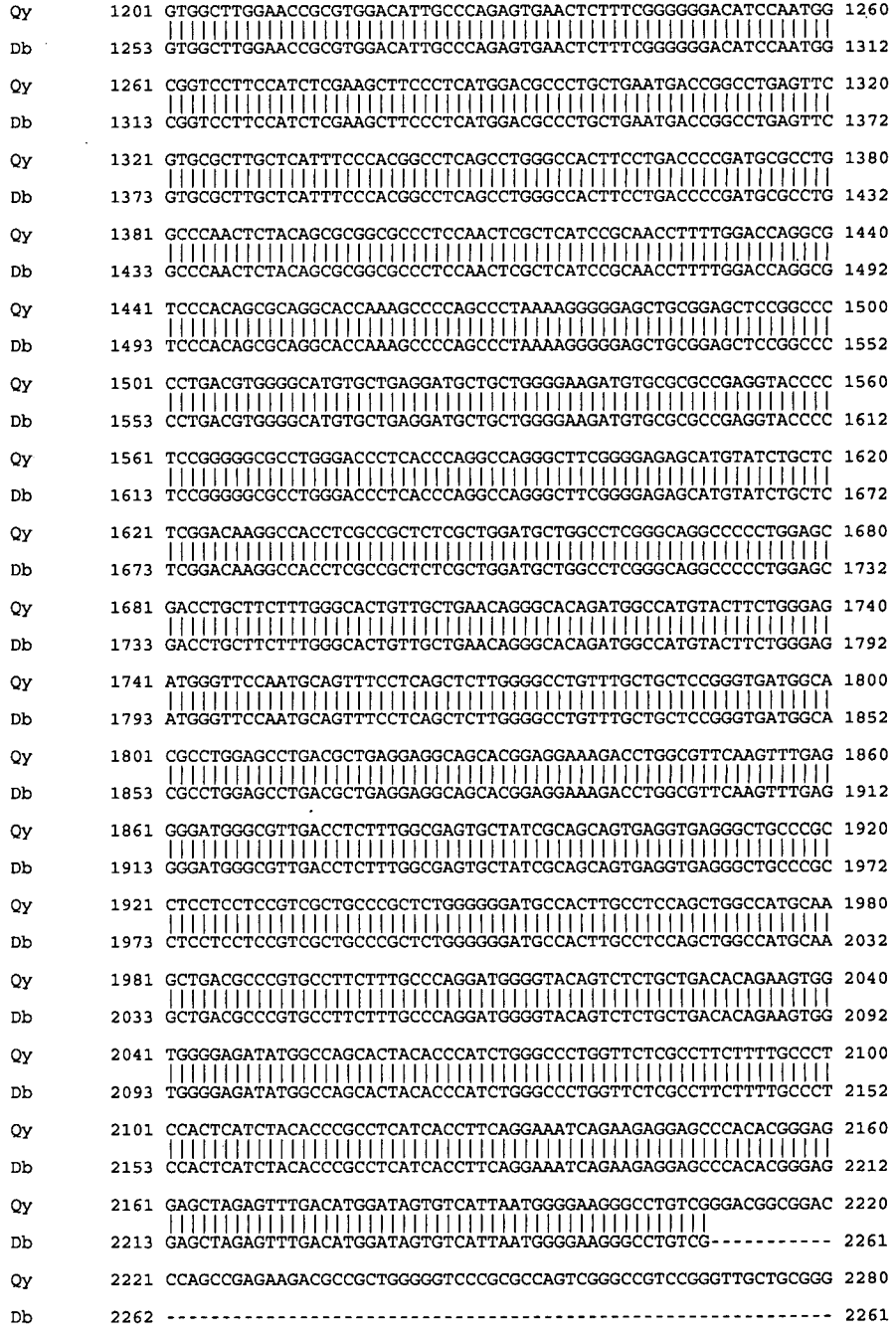
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  AUTHORS   Hofmann,T., Chubanov,V., Gudermann,T. and Montell,C.
  TITLE     TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent
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  JOURNAL   Curr. Biol. 13 (13), 1153-1158 (2003)
  MEDLINE   22726392
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  AUTHORS   Chubanov,V., Hofmann,T., Gudermann,T. and Montell,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAY-2003) Institut fuer Pharmakologie und
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ORIGIN

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Qy       2401 CTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGG 2460
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Qy       2461 GCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTC 2520
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Qy       2521 GCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTC 2580
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Qy       2581 GCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGC 2640
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Qy       2641 TGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATG 2700
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Qy       2701 GTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATC 2760
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Qy       2761 GTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGG 2820
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Qy       2881 AGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAG 2940
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Qy       3001 GCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTG 3060
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Qy       3061 GTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATT 3120
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RESULT 14
MMU575814
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DEFINITION  Mus musculus mRNA for transient receptor potential ion channel
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ACCESSION   AJ575814
VERSION     AJ575814.1  GI:32487285
KEYWORDS    transient receptor potential ion channel melastatin subgroup member
            4 protein; trpm4 gene.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Nilius,B., Prenen,J., Droogmans,G., Voets,T., Vennekens,R.,
            Freichel,M., Wissenbach,U. and Flockerzi,V.
  TITLE     Voltage Dependence of the Ca2+-activated Cation Channel TRPM4
  JOURNAL   J. Biol. Chem. 278 (33), 30813-30820 (2003)
  MEDLINE   22791733
   PUBMED   12799367
REFERENCE   2  (bases 1 to 3800)
  AUTHORS   Vennekens,R. and Freichel,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JUL-2003) Vennekens R., Freichel M., University of
            the Saarland, Institute for Pharmacology and Toxicoloy, 66421
            Homburg - Saar, Saarland, GERMANY
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ORIGIN

  Query Match             66.6%;  Score 2424;  DB 10;  Length 3800;
  Best Local Similarity   79.8%;  Pred. No. 0;
  Matches 2917;  Conservative    0;  Mismatches  710;  Indels   27;  Gaps    4;

Qy          1 ATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAGAAGAAGACCTGC 60
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Qy         61 ACGACGTTCATAGTTGA---CTCCACAGATCCGGGAGGGACCTTGTGCCAGTGTGGGCGC 117
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Qy        118 CCCCGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCCGTGGTGACC 177
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Db        170 CCTCGGGATGCCCACCCTTCTGTGGCTGTGGAGGATGCCTTTGGGGCAGCCGTAGTTACC 229

Qy        178 GTGTGGGACAGCGATGCACACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGAC 237
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Qy        358 TCAGTGCTGGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGT 417
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Qy        418 CGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCAC 477
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Qy        478 ACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGG 537
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Qy        538 GGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACC 597
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Qy        598 CTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGAC 657
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Qy        658 GGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACA 717
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Qy        718 CACGGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAG 777
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Qy        778 CAGAAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGAT 837
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Qy       1018 CCCAAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAG 1077
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AX443225
LOCUS       AX443225               2695 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 7 from Patent WO0210382.
ACCESSION   AX443225
VERSION     AX443225.1  GI:21690620
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wissenbach,U.
  TITLE     Trp8, trp9 and trp10, markers for cancer
  JOURNAL   Patent: WO 0210382-A 7 07-FEB-2002;
            Wissenbach, Ulrich (DE)
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     CDS             303. .2339
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                     /codon_start=1
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                     /db_xref="GI:21690621"
                     /translation="MYLLSDKATSPLSLDAGLGQAPWSDLLLWALLLNRAQMAMYFWE
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                     SPALEHFRVYLSKEAERKLLTWESVHKENFLLARARDKRESDSERLKRTSQKVDLALK
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ORIGIN

  Query Match             62.3%;  Score 2269.4;  DB 6;  Length 2695;
  Best Local Similarity   97.7%;  Pred. No. 0;
  Matches 2335;  Conservative    0;  Mismatches    1;  Indels   55;  Gaps    1;

Qy       1252 ATCCAATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGG 1311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCCAATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGG 60

Qy       1312 CCTGAGTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCG 1371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1372 ATGCGCCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTG 1431
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Qy       2032 CAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTC 2091
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Search completed: June 13, 2005, 02:43:54
Job time : 10276.1 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 16:55:33 ; Search time 7461.25 Seconds
(without alignments)
18579.996 Million cell updates/sec

Title: US-09-869-486B-29_COPY_73_3714
Perfect score: 3642
Sequence: 1 atggtggtgccggagaagga.....acctgcctgggtccaaagac 3642

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1983	54.4	4293	3	AK044094	AK044094 Mus muscu
2	773.6	21.2	912	6	CA488162	CA488162 AGENCOURT
3	719	19.7	879	5	BU858032	BU858032 AGENCOURT
4	697.4	19.1	700	7	CN402549	CN402549 170004706
5	690	18.9	933	5	BQ942718	BQ942718 AGENCOURT
6	666	18.3	894	5	BQ721564	BQ721564 AGENCOURT
7	651.6	17.9	883	5	BQ723742	BQ723742 AGENCOURT
8	646.8	17.8	864	6	CA488844	CA488844 AGENCOURT
9	637.4	17.5	1090	2	BF311909	BF311909 601897749
10	634.4	17.4	672	4	BI759746	BI759746 603045620
11	609.8	16.7	613	5	BX474984	BX474984 DKFZp686M
12	595.4	16.3	804	2	BE905591	BE905591 601495244
13	594.4	16.3	3449	3	AK035197	AK035197 Mus muscu
14	594.4	16.3	3998	3	AK044908	AK044908 Mus muscu
15	584.8	16.1	625	4	BI199159	BI199159 602758878
16	580.2	15.9	599	4	BI910079	BI910079 603067915
17	579	15.9	602	7	CN402548	CN402548 170005322
18	578	15.9	3498	9	AY401205	AY401205 Homo sapi
19	577	15.8	580	5	BP265210	BP265210 BP265210
20	571	15.7	997	2	BF310664	BF310664 601894621
21	568	15.6	587	4	BI010525	BI010525 MR2-EN009
22	560	15.4	892	5	BQ949247	BQ949247 AGENCOURT
23	551	15.1	553	7	CN402551	CN402551 170005977
24	527	14.5	725	7	CK955668	CK955668 4095493 B
25	526	14.4	551	6	CB266373	CB266373 1005278 H
26	521	14.3	582	5	BP351258	BP351258 BP351258
27	509	14.0	582	5	BP280941	BP280941 BP280941
28	504.8	13.9	678	5	BP223875	BP223875 BP223875
29	499.2	13.7	540	7	CN335029	CN335029 170004277
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31	495	13.6	519	4	BI198633	BI198633 602761709
32	485.4	13.3	732	7	CO248115	CO248115 AGENCOURT
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39	452.2	12.4	671	4	BI198267	BI198267 602760054
40	449.2	12.3	3523	3	AK044423	AK044423 Mus muscu
41	447.6	12.3	3498	9	AY401206	AY401206 Pan trogl
42	447.4	12.3	624	7	CK832049	CK832049 4056009 B
43	443	12.2	444	4	BM821224	BM821224 K-EST0090
44	427.2	11.7	869	6	CB193845	CB193845 AGENCOURT
45	412.4	11.3	943	2	BF585270	BF585270 602101933

ALIGNMENTS

RESULT 1
AK044094
LOCUS AK044094 4293 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830089H13 product:similar to TRP-RELATED CATION INFLUX CHANNEL [Homo sapiens], full insert sequence.
ACCESSION AK044094
VERSION AK044094.1 GI:26336171
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 4293)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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ORIGIN

Query Match 54.4%; Score 1983; DB 3; Length 4293;
Best Local Similarity 77.6%; Pred. No. 0;

Matches 2479; Conservative 0; Mismatches 625; Indels 91; Gaps 3;

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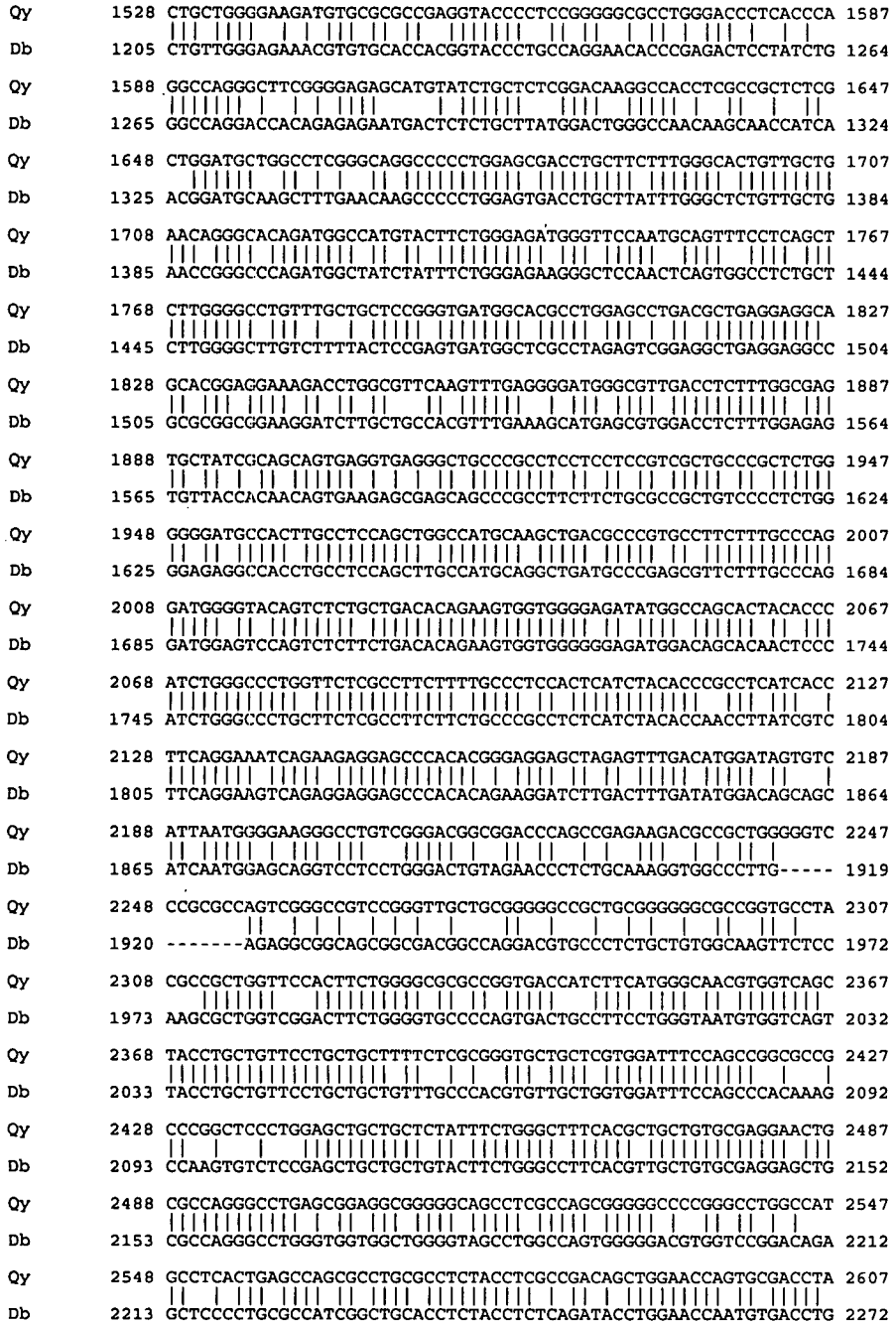
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  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
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  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
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             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
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                     insert size: 1800 bp. Library amplification:  26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee  & Ira Pastan:  Discovery of new breast
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                     Manuscript submitted."
ORIGIN

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RESULT 3
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VERSION     BU858032.1  GI:24043024
KEYWORDS    EST.
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  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 879)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
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             cDNA Library Preparation: Rubin Laboratory
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             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
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                     /db_xref="taxon:9606"
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/clone="IMAGE:6647959"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_107"
/note="Organ: breast; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
ORIGIN

Query Match 19.7%; Score 719; DB 5; Length 879;
Best Local Similarity 96.6%; Pred. No. 8.4e-144;
Matches 799; Conservative 0; Mismatches 20; Indels 8; Gaps 6;

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Qy       2340 GACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGT 2399
             ||||||||||||||| || |||||||||||||||||||||||||||||||||||||||||||
Db          1 GACCATCTTCATGGGCTACCTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGT 60

Qy       2400 GCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTG 2459
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Db         61 GCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTG 120

Qy       2460 GGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCT 2519
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Db        121 GGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCT 180

Qy       2520 CGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCT 2579
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Db        181 CGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCT 240

Qy       2580 CGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGG 2639
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Db        241 CGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGG 300

Qy       2640 CTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCAT 2699
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCAT 360

Qy       2700 GGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGAT 2759
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Db        361 GGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGAT 420

Qy       2760 CGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTG 2819
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Db        421 CGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTG 480

Qy       2820 GCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCC 2879
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCC 540

Qy       2880 AAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCA 2939
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Db        541 AAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCA 600

Qy       2940 GGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCC-GGCTTCT 2998
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Db        601 GGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGGCTTCT 660

Qy       2999 GGGCACACCCTCCTGGGG-CCCAGGCGGGCACCTGCG-TCTCCCAGTATGCCAACT-GGC 3055
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Db        661 GGGCACACCCTCCTGGGGCCCCAGCGGGGCACCTGCGNTCTCCCAGTATGCCCACTGGGC 720

Qy       3056 TGGTGGTGCTGC-TCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTG 3114
             |||||||||||| ||| || ||||||||||||||||||||||||||||||||||||||||
Db        721 TGGTGGTGCTGCTTCCCCGCCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTG 780

Qy       3115 CTCATTGCCATGTTCAGTTACACA---TTCGGCAAAGTACAGGGCAA 3158
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Db        781 CTCATTGCCAATGTTCAGTTAACACATTCCGCCAAAGTACCGGGCCA 827
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RESULT 4
CN402549
LOCUS CN402549 700 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000470662623 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN402549
VERSION CN402549.1 GI:47390143
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 700)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 700 Std Error: 0.00.
FEATURES Location/Qualifiers
source 1. .700
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
H9"
/clone_lib="GRN_ES"
/note="oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
ORIGIN

Query Match 19.1%; Score 697.4; DB 7; Length 700;
Best Local Similarity 99.9%; Pred. No. 3.6e-139;
Matches 698; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        298 GCTGCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTG 357
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Db          2 GCTGCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTG 61

Qy        358 TCAGTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGT 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCAGTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGT 121

Qy        418 CGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCAC 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCAC 181

Qy        478 ACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGG 537
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Db        182 ACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGG 241

Qy        538 GGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACC 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACC 301

Qy        598 CTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGAC 657
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Db        302 CTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGAC 361

Qy        658 GGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACA 717
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Db        362 GGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACA 421
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Qy        718 CACGGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAG 777
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Db        422 CACGGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAG 481

Qy        778 CAGAAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGAT 837
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Db        482 CAGAAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGAT 541

Qy        838 GGTGATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTC 897
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Db        542 GGTGATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTC 601

Qy        898 CTCGTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTG 957
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        602 CTCGTGGCTGGCTCAAGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTG 661

Qy        958 GCCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGA 996
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Db        662 GCCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGA 700


RESULT 5
BQ942718
LOCUS       BQ942718                933 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT_8842138 Lupski_sciatic_nerve Homo sapiens cDNA clone
            IMAGE:6204319 5', mRNA sequence.
ACCESSION   BQ942718
VERSION     BQ942718.1  GI:22358196
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 933)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13625  row: g  column: 08
            High quality sequence stop: 501.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6204319"
                     /sex="male"
                     /tissue_type="sciatic nerve"
                     /dev_stage="adult, 70 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_sciatic_nerve"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.87 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
ORIGIN

  Query Match             18.9%;  Score 690;  DB 5;  Length 933;
  Best Local Similarity   92.3%;  Pred. No. 1.5e-137;
  Matches  783;  Conservative    0;  Mismatches   55;  Indels   10;  Gaps    5;

Qy       1417 ATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAA 1476
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Db          4 ATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAA 63

Qy       1477 GGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGG 1536
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Db         64 GGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGG 123

Qy       1537 AAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGC 1596
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Db        124 AAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGC 183

Qy       1597 TTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCT 1656
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Db        184 TTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCT 243

Qy       1657 GGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCA 1716
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Db        244 GGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCA 303

Qy       1717 CAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCC 1776
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 CAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCC 363

Qy       1777 TGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGG 1836
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGG 423

Qy       1837 AAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGC 1896
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Db        424 AAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGC 483

Qy       1897 AGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCC 1956
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Db        484 AGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCC 543

Qy       1957 ACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTA 2016
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Db        544 ACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAAGATGGGGTA 603

Qy       2017 CAGTCTCTGCTGACACAGAAGTGGT-GGGGAGATATGGCCAGCACTACACCCATCTGGGC 2075
              ||| ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        604 CAGCCTCTGCTGACACAGAAGTGGTGGGGGAGATATGGCCAGCACTACACCCATCTGGGC 663

Qy       2076 CCTGGTTCT-CGCCTTCTTTTGCCCTCCACTCATCTACACCCGCC--TCATCACCTTCAG 2132
              ||||||| | |||||||||||||||||||| ||||| ||||||  |||| |||||| |
Db        664 CCTGGTTTTCCGCCTTCTTTTGCCCTCCACTCTTCTACCCCCGCCCTTCATTACCTTCCG 723

Qy       2133 GAAATCAGAAGAGGAGCCCACAC---GGGAGGAGCTAGAGTTTGACATGGATAGTGTCAT 2189
              |||||||||| | ||| | |   || |||| |   ||  ||  ||| |||| | |
Db        724 GAAATCAGAAAGAGGACCCCCCCCCGGGAGGGAGTTGAGTTTGAACTGGGACAGTGGCTT 783

Qy       2190 TAATGGGGAAGGG---CCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGT 2246
              | |||||| | ||     |    || | |  |||||   ||     ||| ||  | ||||
Db        784 TCATGGGGGAAGGGCCTCGCCTGGAAGGTGGGACCGTTCCACAGGGACCCCCGTTGGGGC 843

Qy       2247 CCCGCGCC 2254
              | | ||||
Db        844 CGCTCGCC 851


RESULT 6
BQ721564
LOCUS       BQ721564                894 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8234684 Lupski_sympathetic_trunk Homo sapiens cDNA clone
            IMAGE:6188589 5', mRNA sequence.
ACCESSION   BQ721564
VERSION     BQ721564.1  GI:21860461
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 894)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13584  row: g  column: 22
            High quality sequence stop: 500.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6188589"
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                     /lab_host="DH10B"
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                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.9 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine); available through Life
                     Technologies."
ORIGIN

  Query Match            18.3%;  Score 666;  DB 5;  Length 894;
  Best Local Similarity  97.3%;  Pred. No. 2.1e-132;
  Matches  720;  Conservative    0;  Mismatches   15;  Indels    5;  Gaps    4;

Qy       1077 GCTCCTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAA 1136
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GGTCCTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAA 69

Qy       1137 GGCCCTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTT 1196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 GGCCCTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTT 129

Qy       1197 GGCTGTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCA 1256
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Db        130 GGCTGTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCA 189

Qy       1257 ATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGA 1316
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Db        190 ATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGA 249

Qy       1317 GTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCG 1376
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Db        250 GTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCG 309

Qy       1377 CCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCA 1436
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Db        310 CCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCA 369

Qy       1437 GGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCG 1496
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Db        370 GGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCG 429

Qy       1497 GCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTA 1556
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Db        430 GCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTA 489

Qy       1557 CCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCT 1616
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Db        490 CCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCT 549

Qy       1617 GCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGG-CCCCCT 1675
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Db        550 GCTCTCGGACAAAGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCCT 609

Qy       1676 GGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCT 1735
              |||||||||||||||||||||||| |||||||||||||||||||||| |||||||||
Db        610 GGAGCGACCTGCTTCTTTGGGCACTGGTGCTGAACAGGGCACAGATGGCCCTGTACTTCT 669

Qy       1736 GGGAGATGGGTTCCAAT-GCAGTTTCCTCAG-CTCTTGGGGCCTGTTTGCTG--CTCCGG 1791
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Db        670 GGGAGATGGGGTCCCATGGCAGTTTCCTCAGCCTCTTGGGGCCCGGTTGCCGGCTCCCGG 729

Qy       1792 GTGATGGCACGCCTGGAGCC 1811
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Db        730 CGGATGGCACCCCCGGAGCC 749


RESULT 7
BQ723742
LOCUS       BQ723742                883 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8241174 Lupski_sympathetic_trunk Homo sapiens cDNA clone
            IMAGE:6186968 5', mRNA sequence.
ACCESSION   BQ723742
VERSION     BQ723742.1  GI:21862639
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 883)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13580  row: d  column: 09
            High quality sequence stop: 557.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6186968"
                     /sex="male"
                     /tissue_type="sympathetic trunk"
                     /dev_stage="adult, 16 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_sympathetic_trunk"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.9 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine); available through Life
                     Technologies."
ORIGIN
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  Query Match             17.9%;  Score 651.6;  DB 5;  Length 883;
  Best Local Similarity   94.3%;  Pred. No. 2.7e-129;
  Matches  709;  Conservative    0;  Mismatches   39;  Indels    4;  Gaps    3;

Qy       1953 TGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGG 2012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGG 60

Qy       2013 GGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTG 2072
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Db         61 GGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTG 120

Qy       2073 GGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACCTTCAG 2132
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Db        121 GGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACCTTCAG 180

Qy       2133 GAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAA 2192
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Db        181 GAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAA 240

Qy       2193 TGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCG 2252
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Db        241 TGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCG 300

Qy       2253 CCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCG 2312
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Db        301 CCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGCCTACGCCG 360

Qy       2313 CTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCT 2372
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Db        361 CTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGCTACCT 420

Qy       2373 GCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGG 2432
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Db        421 GCTGTTCTTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGG 480

Qy       2433 CTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCA 2492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCA 540

Qy       2493 GGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTC 2552
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Db        541 GGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCAGGTCTGGCCATGCCTC 600

Qy       2553 A-CTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGG 2611
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Db        601 ACCTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACAGCGGCGA-CTAGAGG 659

Qy       2612 CTCTCACCTGCTTCCTCCTGGGC--GTGGGCTGCCGGCTGACCCCGGGTTTGTACCACCT 2669
             ||| |||||||||| |||||||||      |     |||  | |||||| | | || || |
Db        660 CTCCCACCTGCTTGCTCCTGGGCCGCGAGCTGCCCGCTTAACCCCGAGATCGTCCCCCTC 719

Qy       2670 GGGCCGCACTGTCCTCTGCATCGACTTCATGG 2701
             ||| | | |||  ||||||| ||  |  ||
Db        720 GGGACCCGCTGGGCTCTGCAAGGAAATTCGGG 751


RESULT 8
CA488844
LOCUS       CA488844                 864 bp    mRNA    linear   EST 14-NOV-2002
DEFINITION  AGENCOURT_10808212 MAPcL Homo sapiens cDNA clone IMAGE:6721042 5',
            mRNA sequence.
ACCESSION   CA488844
VERSION     CA488844.1  GI:24951635
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 864)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Kristi A. Egland, Ira Pastan
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14281  row: i  column: 10
            High quality sequence stop: 571.
FEATURES             Location/Qualifiers
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                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification:  26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee  & Ira Pastan:  Discovery of new breast
                     cancer genes encoding  membrane and secreted proteins..
                     Manuscript submitted."
ORIGIN

  Query Match             17.8%;  Score 646.8;  DB 6;  Length 864;
  Best Local Similarity   94.4%;  Pred. No. 2.9e-128;
  Matches  668;  Conservative    0;  Mismatches   39;  Indels    1;  Gaps    1;

Qy       2894 GCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACG 2953
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACG 60

Qy       2954 TGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTG 3013
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTG 120

Qy       3014 GGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCG 3073
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Db        121 GGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCG 180

Qy       3074 TCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTT 3133
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Qy       3134 ACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCC 3193
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Db        241 ACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCC 300

Qy       3194 TCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACT 3253
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Db        301 TCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACT 360

Qy       3254 TGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGG 3313
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Db        361 TGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGG 420

Qy       3314 CCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGG 3373
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Db        421 CCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGG 480

Qy       3374 AATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACT 3433
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Db        481 AATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACT 540

Qy       3434 CCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACA 3493
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Db        541 CCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACA 600

Qy       3494 TCCGCGAGTACGAACAGCGCCTGAAAGTGCT-GGAGCGGGAGGTCCAGCAGTGTAGCCGC 3552
                |||||||||||||||||||||||||| |||||| ||||||||||||||||||||||  |||
Db        601 TCCGCGAGTACGAACAGCGCCTGANAGTGCTGGGAGCGGGAGGTCCAGCAGTGTACGCGC 660

Qy       3553 GTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCC 3600
                ||  ||| |                |       ||     |||
Db        661 TCCCCTGGGGGTTGNNNNNNNNNNNNNNCCNNNNNCNCCCCCNCCCCC 708


RESULT 9
BF311909
LOCUS       BF311909               1090 bp    mRNA    linear   EST 21-NOV-2000
DEFINITION  601897749F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126764 5',
            mRNA sequence.
ACCESSION   BF311909
VERSION     BF311909.1  GI:11259680
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1090)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM1017  row: b  column: 13
            High quality sequence stop: 633.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_19"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and  Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           17.5%;  Score 637.4;  DB 2;  Length 1090;
  Best Local Similarity   89.6%;  Pred. No. 3.1e-126;
  Matches  757;  Conservative    0;  Mismatches   71;  Indels   17;  Gaps    6;

Qy       1533 GGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCA 1592
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Db          2 GGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCA 61

Qy       1593 GGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGA 1652
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Db         62 GGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGA 121

Qy       1653 TGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAG 1712
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 TGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAG 181

Qy       1713 GGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGG 1772
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Db        182 GGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGG 241

Qy       1773 GGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACG 1832
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Db        242 GGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACG 301

Qy       1833 GAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTA 1892
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Db        302 GAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTA 361

Qy       1893 TCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGA 1952
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGA 421

Qy       1953 TGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGG 2012
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Db        422 TGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGG 481

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Db        482 GGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTG 541

Qy       2073 GGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACCTTCAG 2132
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Qy       2187 CATTAATGGGGAAGGGCCTGTCGGGACGGCGGA---CCCAGCCGAGAAGACGCCGCTGGG 2243
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Db        661 TTACATGGGCGAAGGGGCTGTCCGGGACGGGGAGACCAAGCCGAGGAAGAAGCCGCTGGG 720

Qy       2244 GGTCCCGCG-----CCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCC--GCTGCGGGGGGC 2296
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Db        721 GGTCCCGCGGGCCAAACCGGGGCCGGCACGGGACGCATGGGGGGCCGAGCCAGGAGGGCG 780

Qy       2297 GCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCA 2356
                |||| ||| | ||||   |   ||| |||| || ||||  ||   |  | ||  |||||
Db        781 CCCGGGGCCAAAGCCGGATGGGTCACATCTGAGGGGCGCACGTTGACCACCTCCGGGGCA 840

Qy       2357 ACGTG 2361
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Db        841 ACGGG 845


RESULT 10
BI759746
LOCUS       BI759746               672 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603045620F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185949 5',
            mRNA sequence.
ACCESSION   BI759746
VERSION     BI759746.1  GI:15751324
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 672)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
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           http://image.llnl.gov
           Plate: LLAM11464  row: g  column: 06
           High quality sequence stop: 668.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_116"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female.  Library is
                     oligo-dT primed and  directionally cloned (EcoRV site is
                     destroyed upon cloning).  Average insert size 1.4 kb,
                     insert size range 1-3 kb.  Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber  (Invitrogen).  Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             17.4%;  Score 634.4;  DB 4;  Length 672;
  Best Local Similarity   99.4%;  Pred. No. 1.3e-125;
  Matches  668;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    3;

Qy       2338 GTGACCATCTTCATGGGCAACGTGGTCA-GCTACCTGCTGTTCCTGCTGCTTTTCTCGCG 2396
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Qy       2397 GGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTT 2456
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Db         61 GGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTT 120

Qy       2457 CTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAG 2516
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Db        121 CTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCA-GGCCTGAGCGGAGGCGGGGGCAG 179

Qy       2517 CCTCGCCAGCGGGGGCCCC-GGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCT 2575
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Db        180 CCTCGCCAGCGGGGGCCCCTGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCT 239

Qy       2576 ACCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCG 2635
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Qy       2696 TCATGGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCA 2755
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Qy       2756 AGATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCG 2815
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Db        420 AGATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCG 479

Qy       2816 TGTGGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACT 2875
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Db        480 TGTGGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACT 539

Qy       2876 TCCCAAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTC 2935
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 TCCCAAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTC 599

Qy       2936 CCCAGGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCT 2995
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 CCCAGGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCT 659

Qy       2996 TCTGGGCACACC 3007
```

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             |||||||||| |
Db        660 TCTGGGCACAAC 671


RESULT 11
BX474984
LOCUS       BX474984                613 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp686M22173_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686M22173 5', mRNA sequence.
ACCESSION   BX474984
VERSION     BX474984.1  GI:31669181
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 613)
  AUTHORS   Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     EST (Bahr,A., Lauber,J., Mewes,H.W., Weil,B., et al.)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686M22173) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .613
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686M22173"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="686 (synonym: hlcc3)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

  Query Match             16.7%;  Score 609.8;  DB 5;  Length 613;
  Best Local Similarity   99.7%;  Pred. No. 2.5e-120;
  Matches  611;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2528 GGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACA 2587
             |||| ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          1 GGGGGCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCTCCTCTACCTCGCCGACA 60

Qy       2588 GCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGC 2647
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGC 120

Qy       2648 TGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCA 2707
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCA 180

Qy       2708 CGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCG 2767
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCG 240

Qy       2768 TGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAG 2827
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAG 300

Qy       2828 CCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCC 2887
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCC 360
```

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Qy       2888 TGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACA 2947
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACA 420

Qy       2948 TGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACC 3007
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACC 480

Qy       3008 CTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGC 3067
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGC 540

Qy       3068 TCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGT 3127
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGT 600

Qy       3128 TCAGTTACACATT 3140
             |||||||||||||
Db        601 TCAGTTACACATT 613


RESULT 12
BE905591
LOCUS       BE905591                804 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601495244F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897275 5',
            mRNA sequence.
ACCESSION   BE905591
VERSION     BE905591.1  GI:10398932
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 804)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9691  row: h  column: 12
            High quality sequence stop: 566.
FEATURES             Location/Qualifiers
     source          1. .804
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3897275"
                     /tissue_type="epithelioid carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_70"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match           16.3%;  Score 595.4;  DB 2;  Length 804;
  Best Local Similarity   91.0%;  Pred. No. 3.3e-117;
  Matches  694;  Conservative    0;  Mismatches   51;  Indels   18;  Gaps    5;

Qy       1310 GGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCC 1369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCC 60

Qy       1370 CGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTT 1429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTT 120

Qy       1430 TGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGG 1489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGG 180

Qy       1490 AGCTCCGGCCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGC 1549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGC 240

Qy       1550 CGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCA 1609
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        241 CGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCA-GGCTTCGGGGAGAGCA 299

Qy       1610 TGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGG 1669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 TGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGG 359

Qy       1670 CCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGT 1729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 CCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGT 419

Qy       1730 ACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCC 1789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 ACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCC 479

Qy       1790 GGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGT 1849
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Db        480 GGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCCCGGAGGAAAGACCTGGCGT 539

Qy       1850 TCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCT----------ATCGCAGC 1899
              || ||||||||||||||||||||||||   ||||||||||||         | || |
Db        540 TCCAGTTTGAGGGGATGGGCGTTGACTCTTTTGGCGAGTGCTTTCCGCCAGCACCGGAAG 599

Qy       1900 AGTGAGGTGAGGGCTGCCCGCCTCCTCC--TCCGTCGCTGCCCGCTCTGGGGGGATGCCA 1957
                |||||   || | |||  |||||||  ||  | ||  | | ||| ||||||||||||
Db        600 GTTGAGGGCTGGCCCGCCTTCCTCCTCCCGTCGCTGGCCCCGCTCTCGGGGGGGATGCCA 659

Qy       1958 CTTG--CCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTG---CCCAGGATGG 2012
              ||||  | ||||  ||||||||||||  ||| ||||||||||||||   ||| |  |||
Db        660 CTTGGCCTTCCAAGTGGCCATGCAACTTGAAGCCCGTGCCTTCTTTGCCCCCCGGTGTGG 719

Qy       2013 GGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCC 2055
              ||| ||||||||||| | |  |    | ||||    || | |
Db        720 GGTCCAGTCTCTGCTGGCCCCCACACTGGGGGGGCGGATTGGC 762


RESULT 13
AK035197
LOCUS       AK035197                3449 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 12 days embryo embryonic body between diaphragm region
            and neck cDNA, RIKEN full-length enriched library, clone:9430099A16
            product:transient receptor potential cation channel, subfamily M,
            member 5, full insert sequence.
ACCESSION   AK035197
VERSION     AK035197.1  GI:26330491
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
```

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  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3449)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:9430099A16"
                     /db_xref="taxon:10090"
                     /clone="9430099A16"
                     /tissue_type="embryonic body between diaphragm region and
                     neck"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="12 days embryo"
     CDS             <1. .3094
                     /note="unnamed protein product; putative
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                     member 5 (MGD|MGI:1861718, GB|NM_020277, evidence: BLASTN,
                     99%, match=3363)"
                     /codon_start=2
                     /protein_id="BAC28976.1"
                     /db_xref="GI:26330492"
                     /translation="RAPAWRAQHSKAQPKLLLRSLPPPLSLAQEDTPIHYPADEGNIQ
                     GPLCPLDSNLSHFILVESGALGSGNDGLTELQLSLEKHISQQRTGYGGTSCIQIPVLC
                     LLVNGDPNTLERISRAVEQAAPWLILAGSGGIADVLAALVSQPHLLVPQVAEKQFREK
                     FPSECFSWEAIVHWTELLQNIAAHPHLLTVYDFEQEGSEDLDTVILKALVKACKSHSQ
                     EAQDCLDELKLAVAWDRVDIAKSEIFNGDVEWKSCDLEEVMTDALVSNKPDFVRLFVD
                     SGADMAEFLTYGRLQQLYHSVSPKSLLFELLQRKHEEGRLTLAGLGAQQARELPIGLP
                     AFSLHEVSRVLKDFLHDACRGFYQDGRRMEERGPPKRPAGQKWLPDLSRKSEDPWRDL
                     FLWAVLQNRYEMATYFWAMGREGVAAGLAACKIIKEMSHLENEAEVARTMREAKYEQL
                     ALDLFSECYGNSEDRAFALLVRRNHSWSRTTCLHLATEADAKAFFAHDGVQAFLTKIW
                     WGDMATGTPILRLLGAFTCPALIYTNLISFSEDAPQRMDLEDLQEPDSLDMEKSFLCS
                     RGGQLEKLTEAPRAPGDLGPQAAFLLTRWRKFWGAPVTVFLGNVVMYFAFLFLFTYVL
                     LVDFRPPPQGPSGSEVTLYFWVFTLVLEEIRQGFFTDEDTHLVKKFTLYVEDNWNKCD
                     MVAIFLFIVGVTCRMVPSVFEAGRTVLAIDFMVFTLRLIHIFAIHKQLGPKIIIVERM
                     MKDVFFFLFFLSVWLVAYGVTTQALLHPHDGRLEWIFRRVLYRPYLQIFGQIPLDEID
                     EARVNCSLHPLLLESSASCPNLYANWLVILLLVTFLLVTNVLLMNLLIAMFSYTFQVV
                     QGNADMFWKFQRYHLIVEYHGRPALAPPFILLSHLSLVLKQVFRKEAQHKRQHLERDL
                     PDPLDQKIITWETVQKENFLSTMEKRRRDSEGEVLRKTAHRVDLIAKYIGGLREQEKR
                     IKCLESQANYCMLLLSSMTDTLAPGGTYSSSQNCGCRSQPASARDREYLESGLPPSDT
                     "
ORIGIN

  Query Match           16.3%;  Score 594.4;  DB 3;  Length 3449;
  Best Local Similarity   53.9%;  Pred. No. 6.6e-117;
  Matches 1590;  Conservative    0;  Mismatches 1236;  Indels  124;  Gaps   13;

Qy        656 ACGGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCA 715
              | ||   ||  |  |||||||||  |||   |||   |||| |||| |||||    |||
Db        132 AGGGACCCCTCTGCCCCCTGGACAGCAATCTCTCCCACTTCATCCTTGTGGAGTCAGGCG 191

Qy        716 CACACGGCTGCCTG---GGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCT 772
              | |  ||  |  |   |  ||   ||     | |   || ||||||||    ||||||
Db        192 CCCTTGGGAGTGGGAACGACGGGCTGACAGAGCTGCAGCTGAGCCTGGAGAAGCACATCT 251

Qy        773 CACAGCAGAAGACGGGCGTGGGAGGGACTGGA---ATTGACATCCCTGTCCTGCTCCTCC 829
              | ||||||| ||| ||    || || ||  |    ||  | || ||||||||   |||
Db        252 CTCAGCAGAGGACAGGTTATGGGGGCACCAGCTGCATCCAGATACCTGTCCTTTGCCTGT 311

Qy        830 TGATTGATGGTGATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCC 889
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Db        312 TGGTCAATGGTGACCCCAACACCCTAGAGAGGATTTCCAGGGCAGTGGAGCAGGCTGCCC 371

Qy        890 CATGTCTCCTCGTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAG 949
              |||| ||  || |||| || || || ||  ||| ||    || || |     ||
Db        372 CATGGCTGATCCTGGCAGGTTCTGGTGGCATTGCTGATGTACTCGCTGCCCTGGTGAGCC 431

Qy        950 ACACTCTGGCCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGC 1009
              |  |||    ||  | |     || ||  | |                |     |||
Db        432 AGCCTCATCTCCTGGTGCCCCAGGTGGCTGAGAAGCAGTTCAGAGAGAAATTCCCCAGCG 491

Qy       1010 GTTTCTTTCCCAAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCC 1069
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Db        492 AGTGTTTCTCTTGGGAAGCCATTGTACACTGGACAGAGCTGTTACAGAACATTGCTGCAC 551

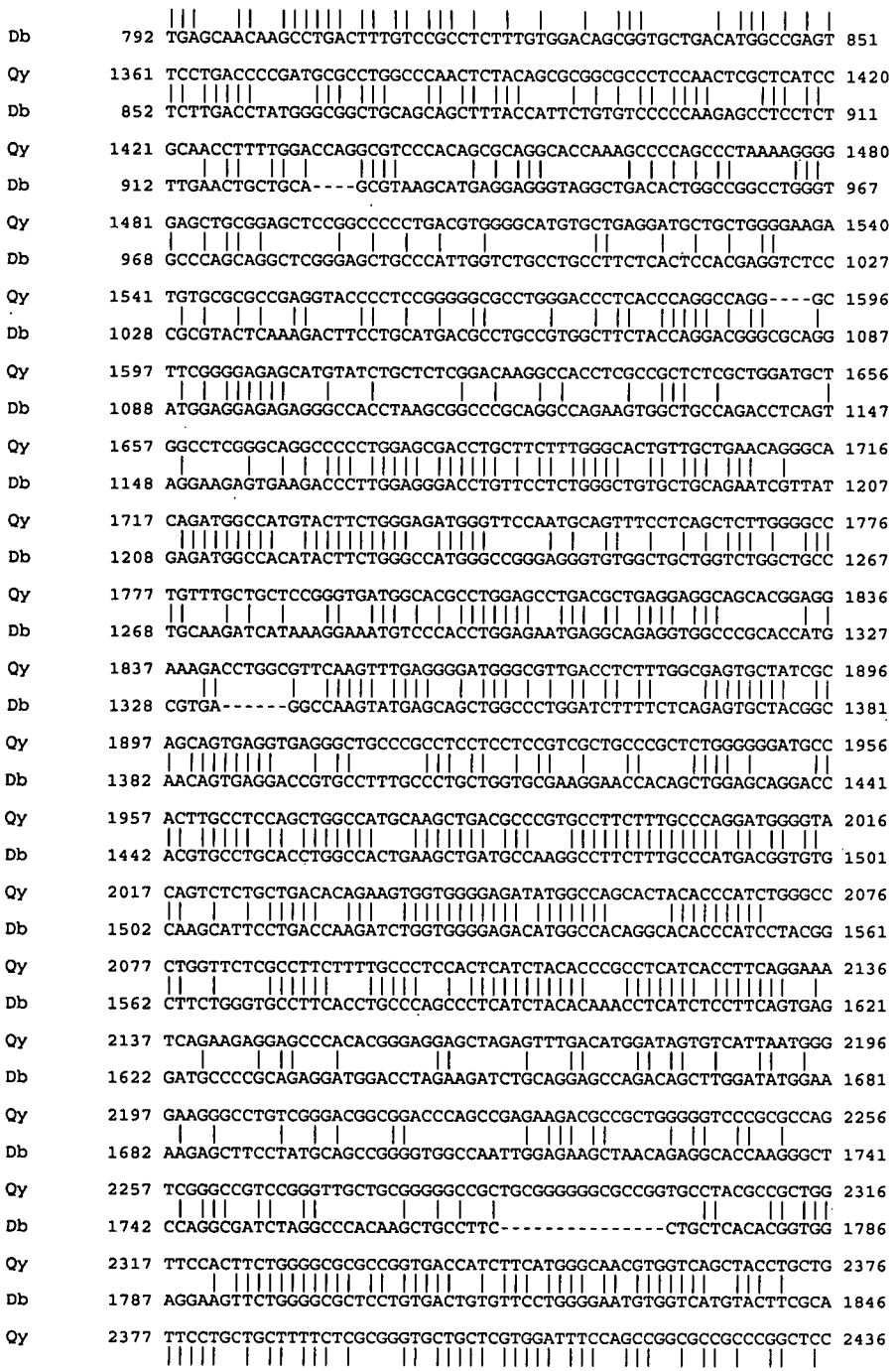
Qy       1070 GGAAGGAGCTCCTGACAGTCTATTCTTCTG---AGGATGGGTCTGAGGAATTCGAGACCA 1126
                | || || ||||| |||   |  |   |||| || || ||||| || || ||
Db        552 ACCCCCACCTGCTCACAGTATATGACTTCGAGCAGGAGGGTTCGGAGGACTTGGACACTG 611

Qy       1127 TAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGG------AGCTCGGAGGCCTCAGCCTACC 1180
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Db        612 TCATCCTCAAGGCACTTGTGAAAGCCTGCAAGAGCCACAGCCAAGAAGCCCAAGACTGCC 671

Qy       1181 TGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCT 1240
              | ||||||||    || || ||||| ||| | ||||||||||||||| ||||||| |||
Db        672 TAGATGAGCTCAAGTTAGCAGTGGCCTGGGATCGCGTGGACATTGCCAAGAGTGAAATCT 731

Qy       1241 TTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGC 1300
              |    |||||| |  ||||| |||||    |  | ||||      | |  || |||||
Db        732 TCAATGGGGACGTGGAATGGAAGTCCTGTGACTTGGAAGAGGTGATGACAGATGCCCTCG 791

Qy       1301 TGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACT 1360
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Db 792 TGAGCAACAAGCCTGACTTTGTCCGCCTCTTTGTGGACAGCGGTGCTGACATGGCCGAGT 851
Qy 1361 TCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCC 1420
Db 852 TCTTGACCTATGGGCGGCTGCAGCAGCTTTACCATTCTGTGTCCCCCAAGAGCCTCCTCT 911
Qy 1421 GCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGG 1480
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Qy 2017 CAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCATCTGGGCC 2076
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DEFINITION Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone:B130011E10 product:transient receptor potential cation channel, subfamily M, member 5, full insert sequence.
ACCESSION AK044908
VERSION AK044908.1 GI:26090604
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3998)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. Tomohiro Kono (Department of Animal Science, Tokyo University of Agriculture, 1737 Hunako Atsugi City, Kanagawa Prefecture, Japan) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
FEATURES Location/Qualifiers
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misc_feature 1. .3998
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ORIGIN

Query Match 16.3%; Score 594.4; DB 3; Length 3998;
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Matches 1590; Conservative 0; Mismatches 1236; Indels 124; Gaps 13;

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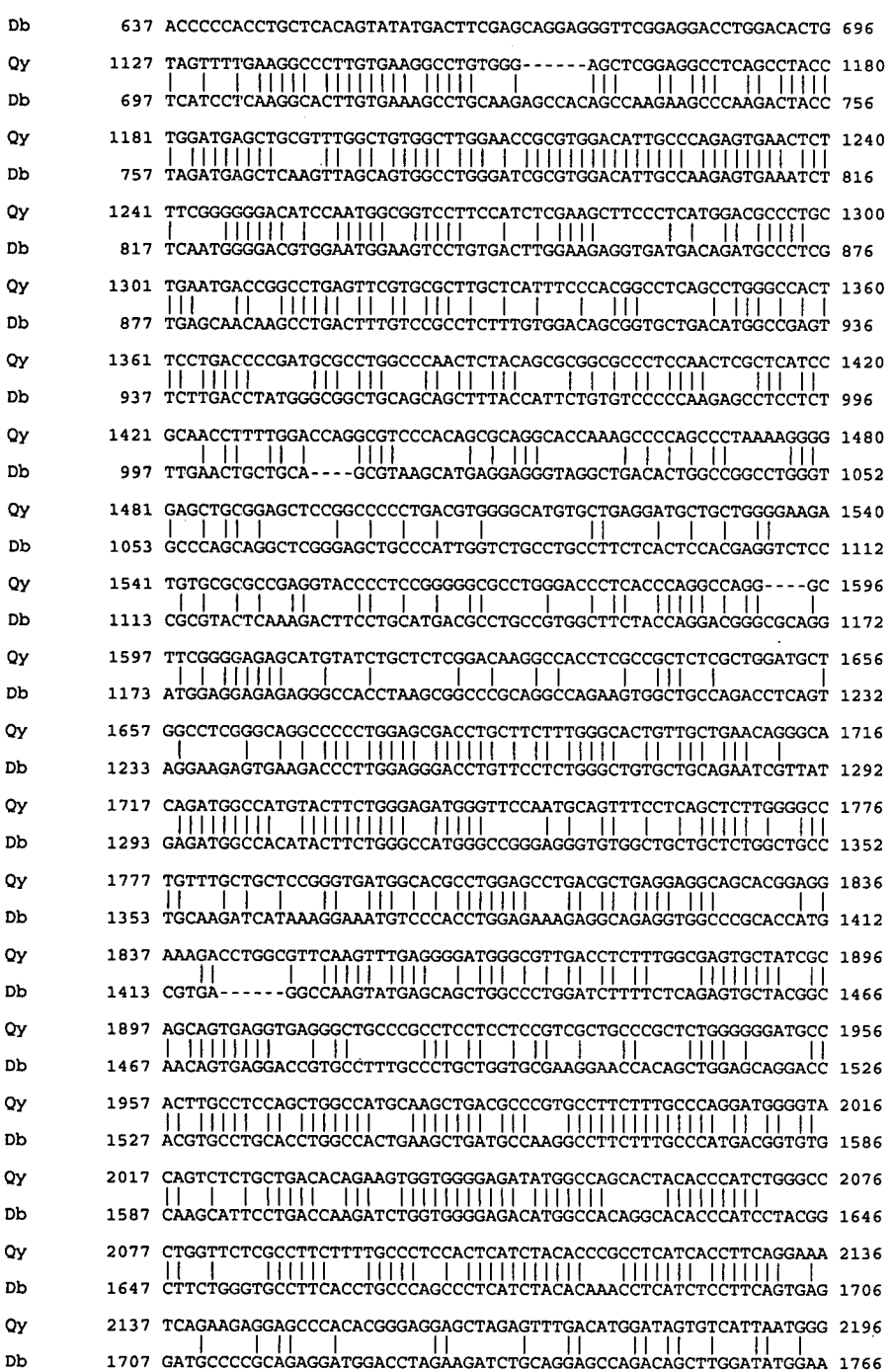
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REFERENCE   1  (bases 1 to 625)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM1777  row: l  column: 19
            High quality sequence stop: 618.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:4894242"
                     /tissue_type="neuroblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_19"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and  Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN
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  Query Match             16.1%;  Score 584.8;  DB 4;  Length 625;
  Best Local Similarity   99.2%;  Pred. No. 6e-115;
  Matches  619;  Conservative    0;  Mismatches    2;  Indels    3;  Gaps    3;
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Qy       1651 GATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAAC 1710
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Qy       1711 A-GGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCAGCTCT 1769
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Qy       1770 TGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGC 1829
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Qy       2010 TGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACACCCAT 2069
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Search completed: June 13, 2005, 08:20:58
Job time : 7470.25 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 04:57:16 ; Search time 1216.46 Seconds
(without alignments)
17723.358 Million cell updates/sec

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Perfect score: 3642
Sequence: 1 atggtggtgccggagaagga.....acctgcctgggtccaaagac 3642

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3642	100.0	4061	3	AAA49923	Aaa49923 Human cal
2	3642	100.0	4061	10	ADH62711	Adh62711 Ca activa
3	3642	100.0	4061	13	ADR73511	Adr73511 Human TRP
4	3642	100.0	4061	13	ADS12774	Ads12774 Transient
5	3640.4	100.0	4042	6	AAD32372	Aad32372 Human Trp
6	3498	96.0	3501	6	ABK92224	Abk92224 Prostate
7	3498	96.0	3501	11	ADN39597	Adn39597 Cancer/an
8	3498	96.0	4641	11	ADN39239	Adn39239 Cancer/an
9	3473.8	95.4	3898	12	ADL06463	Adl06463 Human tum
10	3421.2	93.9	3810	6	ABK92167	Abk92167 Prostate
11	3421.2	93.9	3810	13	ADR66772	Adr66772 Human pro
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16	3374.4	92.7	3900	12	ADH51622	Adh51622 Human 186
17	3373.8	92.6	3387	5	AAH76384	Aah76384 Human TLC
18	3373.8	92.6	3390	12	ADH51624	Adh51624 Human 186
19	3253.4	89.3	3599	6	ABK28677	Abk28677 Human cDN
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21	3199.8	87.9	3676	13	ADQ85834	Adq85834 Human tum
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25	2269.4	62.3	2695	6	AAD32373	Aad32373 Human Trp
26	2073.4	56.9	2459	12	ADL06424	Adl06424 Human tum
27	1911	52.5	2393	2	AAV26656	Aav26656 Human PS1
28	1911	52.5	2393	3	AAA64090	Aaa64090 Consensus
29	1892.2	52.0	2180	3	AAA49921	Aaa49921 Human cal
30	1240.8	34.1	2176	12	ADQ96621	Adq96621 Human PS1
31	1158	31.8	1524	2	AAV58585	Aav58585 Prostate
32	1158	31.8	1524	2	AAV61200	Aav61200 Full leng
33	1158	31.8	1524	3	AAA06348	Aaa06348 Human imm
34	1158	31.8	1524	3	ABS71253	Abs71253 Human pro
35	1158	31.8	1524	4	AAH93464	Aah93464 Human pro
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37	1158	31.8	1524	4	AAH02529	Aah02529 Prostate
38	1158	31.8	1524	4	AAH84778	Aah84778 Human pro
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40	1158	31.8	1524	5	AAS10107	Aas10107 Human pro
41	1158	31.8	1524	6	ABL94928	Abl94928 Human J1-
42	1158	31.8	1524	6	ABS58637	Abs58637 Prostate
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ALIGNMENTS

RESULT 1
AAA49923
ID AAA49923 standard; cDNA; 4061 BP.
XX
AC AAA49923;
XX
DT 10-OCT-2000 (first entry)
XX
DE Human calcium channel SOC-3/CRAC-2 cDNA.
XX
KW SOC-2/CRAC-1; calcium channel; human; store operated channel;
KW calcium release activated channel; therapy; diagnosis;
KW lymphocyte proliferative disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 382. .5979
FT /*tag= a
XX
PN WO200040614-A2.
XX
PD 13-JUL-2000.
XX
PF 20-DEC-1999; 99WO-US029996.
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PR 30-DEC-1998; 98US-0114220P.
PR 29-JAN-1999; 99US-0120018P.
PR 22-JUN-1999; 99US-0140415P.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Scharenberg AM;
XX
DR WPI; 2000-465957/40.
DR P-PSDB; AAY95436.
XX
PT New SOC/CRAC calcium channel polynucleotides and polypeptides used to
PT diagnose and treat proliferative disorders associated with the channel,
PT and to screen for novel modulators of the channel.
XX
PS Claim 1(a); Page 99-100; 108pp; English.
XX

CC The present sequence is a full-length nucleotide sequence of human SOC-
CC 3/CRAC-2 cDNA. It includes an open reading frame encoding SOC-3/CRAC-2
CC (see AAY95436), a member of a novel family of store operated channel
CC (SOC) or calcium release activated channel (CRAC) polypeptides that
CC modulate Ca2+ flux into and out of a cell, and which may be activated
CC upon depletion of Ca2+ from intracellular calcium stores, allowing Ca2+
CC influx into a cell. SOC-3/CRAC-2 is expressed predominantly in kidney and
CC colon. Compositions for expressing SOC/CRAC calcium channel polypeptides
CC in cells may be useful for treating patients that have reduced
CC extracellular calcium influx into their SOC/CRAC-expressing cells. They
CC will also be useful for delivering therapeutic and/or imaging agents to
CC such cells to modulate proliferation and growth. SOC/CRAC polypeptides
CC also represent targets for designing and/or identifying inhibitors that
CC block lymphocyte proliferation and binding agents that selectively bind
CC to SOC/CRAC polypeptides to which drugs or toxins can be conjugated for
CC delivery to SOC/CRAC expressing cells. SOC/CRAC polynucleotides are used
CC as probes and primers to identify other members of the SOC/CRAC family of
CC calcium channels, as diagnostic reagents for identifying the presence of
CC SOC/CRAC polypeptides in biological samples, as agents for generating
CC SOC/CRAC binding polypeptides, and in gene therapy. Methods for
CC determining the level of SOC/CRAC expression in a subject can be used to
CC assess the presence, or absence, of stage of a proliferative disorder,
CC e.g. a lymphocyte proliferative disorder
XX
SQ Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

Query Match 100.0%; Score 3642; DB 3; Length 4061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3642; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        781 AAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGT 840
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Db        853 AAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGT 912

Qy        841 GATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTC 900
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Qy        901 GTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCC 960
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Qy       2161 GAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGAC 2220
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Db       2533 GCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTC 2592

Qy       2521 GCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTC 2580
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Db       2593 GCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTC 2652

Qy       2581 GCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGC 2640
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Qy       2641 TGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATG 2700
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Qy       2701 GTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATC 2760
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Qy       2821 CTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCA 2880
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Qy       2881 AGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAG 2940
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Qy       3061 GTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATT 3120
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Qy       3121 GCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCG 3180
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Qy       3241 GTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAG 3300
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Qy       3361 CTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAG 3420
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Qy       3421 CGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAA 3480
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Qy       3481 CAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAG 3540
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Qy       3601 CCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGAC 3642
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Db       3673 CCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGAC 3714
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RESULT 2
ADH62711
ID ADH62711 standard; cDNA; 4061 BP.
XX
AC ADH62711;
XX
DT 25-MAR-2004 (first entry)
XX
DE Ca activated nonselective transmembrane channel protein TRPM4b cDNA.
XX
KW bioactive agent; monovalent cation permeability; TRPM4b channel; human;
KW calcium activated nonselective transmembrane channel; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   73. .3717

```
FT                  /*tag=  a
FT                  /product= "TRPM4b"
FT                  /note= "Calcium activated nonselective (CAN)
FT                  transmembrane channel protein"
XX
PN   US2003143557-A1.
XX
PD   31-JUL-2003.
XX
PF   08-MAY-2002; 2002US-00142649.
XX
PR   25-JAN-2002; 2002US-0351938P.
PR   02-MAY-2002; 2002US-0377937P.
XX
PA   (PENN/) PENNER R.
XX
PI   Penner R;
XX
DR   WPI; 2003-829785/77.
DR   P-PSDB; ADH62712.
XX
PT   Screening for candidate bioactive agents involves contacting calcium-
PT   activated nonselective transmembrane channel polypeptide designated as
PT   TRPM4b with candidate agent, determining binding of candidate agent
PT   TRPM4b.
XX
PS   Claim 5; SEQ ID NO 1; 25pp; English.
XX
CC   The invention describes a method of screening (M1) for a candidate
CC   bioactive agent (CA) modulating monovalent cation (MC) permeability of
CC   the TRPM4b (I) channel. The method involves providing a recombinant cell
CC   (RC) with a nucleic acid encoding (I) and an inducible promoter operably
CC   linked to (I), capable of expressing (I), and comprises an MC indicator,
CC   inducing RC to express (I), contacting RC with MC and CA, and detecting
CC   intracellular levels of MC with an indicator. The method is useful for
CC   creening for a candidate bioactive agent capable of modulating monovalent
CC   cation permeability of a TRPM4b channel. This sequence encodes human
CC   calcium activated nonselective (CAN) transmembrane channel protein
CC   TRPM4b.
XX
SQ   Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 3642;  DB 10;  Length 4061;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3642;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAGAAGAAGACCTGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 ATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAGAAGAAGACCTGC 132

Qy         61 ACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAGTGTGGGCGCCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 CGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCCGTGGTGACCGTG 180
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Qy        181 TGGGACAGCGATGCACACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTC 240
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Qy        241 ACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCT 300
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Qy        301 GCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCA 360
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Qy        421 GGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACG 480
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Db        493 GGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACG 552

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Qy        541 ACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTC 600
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Qy        601 ATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGG 660
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Qy        661 GTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACAC 720
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Db        733 GTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACAC 792

Qy        721 GGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAG 780
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Db        793 GGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAG 852

Qy        781 AAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGT 840
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Qy        901 GTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCC 960
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Qy        961 CCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCC 1020
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Qy       1141 CTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCT 1200
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Qy       1201 GTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGG 1260
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Qy       1501 CCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCC 1560
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Qy       1981 GCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGG 2040
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Qy       2101 CCACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAG 2160
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Qy       2401 CTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGG 2460
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Db       2533 GCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTC 2592

Qy       2521 GCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTC 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2593 GCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTC 2652

Qy       2581 GCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2653 GCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGC 2712

Qy       2641 TGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATG 2700
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Db       2713 TGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATG 2772

Qy       2701 GTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATC 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2773 GTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATC 2832

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Db       2833 GTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGG 2892

Qy       2821 CTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCA 2880
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Db       2953 AGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAG 3012

Qy       2941 GAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGG 3000
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Db       3013 GAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGG 3072

Qy       3001 GCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3073 GCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTG 3132

Qy       3061 GTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATT 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3133 GTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATT 3192

Qy       3121 GCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCG 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3193 GCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCG 3252

Qy       3181 CAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATC 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3253 CAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATC 3312

Qy       3241 GTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAG 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3313 GTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAG 3372

Qy       3301 CCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAG 3360
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Db       3373 CCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAG 3432

Qy       3361 CTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3433 CTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAG 3492

Qy       3421 CGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAA 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3493 CGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAA 3552

Qy       3481 CAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAG 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3553 CAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAG 3612

Qy       3541 CAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCC 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3613 CAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCC 3672

Qy       3601 CCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGAC 3642
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Db       3673 CCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGAC 3714

RESULT 3
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ADR73511
ID   ADR73511 standard; DNA; 4061 BP.
XX
AC   ADR73511;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human TRPM4, gene.
XX
KW   TRPM4; apoptosis; inhibitor; tumour; cytostatic; cancer; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             73. .3717
FT                   /*tag=  a
FT                   /product= "Human TRPM4"
XX
PN   WO2004076682-A2.
XX
PD   10-SEP-2004.
XX
PF   26-FEB-2004; 2004WO-US006020.
XX
PR   26-FEB-2003; 2003US-0450886P.
XX
PA   (SURR-) SURROMED INC.
XX
PI   Axenovich SA,  Stull R,  Gelman M,  Chui K,  Ng D;
XX
DR   WPI; 2004-653428/63.
DR   P-PSDB; ADR73512.
XX
PT   Identifying a compound for inducing apoptosis, useful for diagnosing and
PT   treating cancer, comprises identifying an inhibitor of a target.
XX
PS   Example 1; SEQ ID NO 79; 255pp; English.
XX
CC   The invention relates to a novel method for identifying a compound for
CC   inducing apoptosis comprises identifying an inhibitor of a target.
CC   Examples of an inhibitor of a target include: angio-associated, migratory
CC   cell protein (AAMP), disintegrin and metalloproteinase domain 8 (ADAM8),
CC   disintegrin-like and metalloprotease (reporlysin type) with
CC   thrombospondin type 1 motif, 17 (ADAMTS17), adenylate cyclase 3 (ADCY3),
CC   adrenergic beta receptor kinase 1 (ADRBK1), bladder cancer associated
CC   protein (BLCAP), chromosome 22 open reading frame 5 (C22orf5), CD81
CC   antigen (target of antiproliferative antibody 1 (CD81), CD9 antigen (p24)
CC   (CD9), claudin 4 (CLDN4), chloride intracellular channel 1 (CLIC1),
CC   collagen, type VI, alpha 2 (COL6A2), CTL2, endothelin converting enzyme 1
CC   (ECE1), ephrinB1 (EFNB1), flotillin 2 (FLOT2), intercellular adhesion
CC   molecule 3 (ICAM3), iduronate 2-sulfatase (Hunter syndrome) (IDS), jagged
CC   2 (JAG2), junctional adhesion molecule 1 (JAM1), lectin, galactoside-
CC   binding soluble 3 binding protein (LGALS3BP), similar to possible G-
CC   protein receptor (LOC146330), CGI-78 protein (LOC51107), lipoprotein
CC   lipase (LPL), low density lipoprotein receptor-related protein 5 (LRP5),
CC   Lutheran blood group (Auberger b antigen included) (LU), membrane
CC   component, chromosome11, surface marker 1 (M11S1), serum constituent
CC   protein (MSE55), neuropathy target esterase (NTE), Homo sapiens cDNA
CC   FL31043 fis, clone HSYRA2000248 (PLEXIN A1) or Homo sapiens cDNA FLJ44113
CC   fis, clone TESTI4046487, highly similar to Mus musculus plexin A1
CC   (PLXNA1), protein tyrosine phosphatase, receptor type, f polypeptide
CC   (PTPRF), interacting protein (liprin), alpha 3 (PPFIA3), Homo sapiens
CC   peptide-histidine transporter 4 (PTR4), mRNA (PTR4), solute carrier
CC   family 16 (monocarboxylic acid transporters) member 3 (SLC16A3), solute
CC   carrier family 1 (neutral amino acid transporter) member 5 (SLC1A5),
CC   solute carrier family 39 (zinc transporter) member 3 (SLC39A1), serine
CC   protease inhibitor, Kunitz type 2 (SPINT2), stanniocalcin 2 (STC2),
CC   tumour necrosis receptor superfamily member 21 (TNFRSF21), tumour
CC   rejection antigen (gp96) 1 (TRA1), or transient receptor potential cation
CC   channel, subfamily M member 4 (TRPM4), respectively comprising any of the
CC   40 sequences of 87-1615 amino acids (the even numbers selected from SEQ
CC   ID:2-80), shown in the specification. The invention further comprises a
CC   method for inducing apoptosis and a method for diagnosing a tumour. The
CC   novel compounds have cytostatic activity. The method is useful for
CC   identifying a compound for inducing apoptosis. The methods and compounds
CC   are useful for diagnosing and treating cancer, and in determining the
CC   prognosis for cancer in the patient or the susceptibility of the patient
CC   to a therapeutic treatment. This polynucleotide sequence represents a
CC   gene encoding one of the 40 protein targets of the invention.
XX
SQ   Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 3642;  DB 13;  Length 4061;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3642;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAGAAGAAGACCTGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 ATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAGAAGAAGACCTGC 132

Qy         61 ACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAGTGTGGGCGCCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 ACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAGTGTGGGCGCCCC 192

Qy        121 CGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCCGTGGTGACCGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 CGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCCGTGGTGACCGTG 252

Qy        181 TGGGACAGCGATGCACACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 TGGGACAGCGATGCACACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTC 312

Qy        241 ACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 ACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCT 372

Qy        301 GCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 GCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCA 432

Qy        361 GTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 GTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGT 492

Qy        421 GGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 GGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACG 552

Qy        481 GGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        541 ACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTC 600
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Qy        601 ATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGG 660
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Db        673 ATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGG 732

Qy        661 GTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACAC 720
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Db        733 GTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACAC 792

Qy        721 GGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 GGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAG 852

Qy        781 AAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        853 AAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGT 912

Qy        841 GATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 GATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTC 972
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Qy       901 GTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCC 960
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Db       973 GTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCC 1032

Qy       961 CCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCC 1020
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Db      1033 CCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCC 1092

Qy      1021 AAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTC 1080
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Db      1093 AAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTC 1152

Qy      1081 CTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCC 1140
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Qy      1141 CTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCT 1200
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Qy      1201 GTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGG 1260
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Qy      1261 CGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTC 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1333 CGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTC 1392

Qy      1321 GTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTG 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1393 GTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTG 1452

Qy      1381 GCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCG 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1453 GCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCG 1512

Qy      1441 TCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCC 1500
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Qy      1501 CCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCC 1560
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Db      1573 CCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCC 1632

Qy      1561 TCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTC 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1633 TCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTC 1692

Qy      1621 TCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGC 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1693 TCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGC 1752

Qy      1681 GACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAG 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1753 GACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAG 1812

Qy      1741 ATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCA 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1813 ATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCA 1872

Qy      1801 CGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAG 1860
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Db      1873 CGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAG 1932

Qy      1861 GGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGC 1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      1921 CTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAA 1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      1981 GCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGG 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2053 GCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGG 2112

Qy      2041 TGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCT 2100
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Db      2113 TGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCT 2172

Qy      2101 CCACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAG 2160
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Db      2173 CCACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAG 2232

Qy      2161 GAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGAC 2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2233 GAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGAC 2292

Qy      2221 CCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGG 2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2293 CCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGG 2352

Qy      2281 GGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTG 2340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2353 GGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTG 2412

Qy      2341 ACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTG 2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2413 ACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTG 2472

Qy      2401 CTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGG 2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2473 CTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGG 2532

Qy      2461 GCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTC 2520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2533 GCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTC 2592

Qy      2521 GCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTC 2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2593 GCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTC 2652

Qy      2581 GCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGC 2640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2653 GCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGC 2712

Qy      2641 TGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATG 2700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2713 TGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATG 2772

Qy      2701 GTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATC 2760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2773 GTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATC 2832

Qy      2761 GTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGG 2820
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2833 GTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGG 2892

Qy      2821 CTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCA 2880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2893 CTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCA 2952

Qy      2881 AGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAG 2940
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2953 AGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAG 3012

Qy      2941 GAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGG 3000
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3013 GAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGG 3072

Qy      3001 GCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTG 3060
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3073 GCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTG 3132

Qy      3061 GTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATT 3120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3133 GTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATT 3192

Qy       3121 GCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCG 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3193 GCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCG 3252

Qy       3181 CAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATC 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3253 CAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATC 3312

Qy       3241 GTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAG 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3313 GTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAG 3372

Qy       3301 CCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAG 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3373 CCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAG 3432

Qy       3361 CTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3433 CTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAG 3492

Qy       3421 CGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAA 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3493 CGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAA 3552

Qy       3481 CAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAG 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3553 CAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAG 3612

Qy       3541 CAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCC 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3613 CAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCC 3672

Qy       3601 CCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGAC 3642
             |||||||||||||||||||||||||||||||||||||||||||
Db       3673 CCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGAC 3714
```

RESULT 4
ADS12774

```
ID   ADS12774 standard; cDNA; 4061 BP.
XX
AC   ADS12774;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Transient receptor potential cation channel, subfamily M member 4b cDNA.
XX
KW   transient receptor potential cation channel; subfamily M; member 4;
KW   TRPM4; phospholipase A1-A; PLA1A; butyryl coenzyme A synthetase 1; BUCS1;
KW   prostate cancer; TRPM4b; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             73. .3717
FT                   /*tag= a
FT                   /product= "Human TRPM4b protein"
XX
PN   JP2004267118-A.
XX
PD   30-SEP-2004.
XX
PF   10-MAR-2003; 2003JP-00063578.
XX
PR   10-MAR-2003; 2003JP-00063578.
XX
PA   (SANY ) SANKYO CO LTD.
XX
DR   WPI; 2004-693915/68.
DR   P-PSDB; ADS12775.
XX
PT   Detecting prostatic cancer, comprises extracting RNA fractions from test
PT   substance of subject and normal human, measuring and analyzing the
PT   difference in e.g., phospholipase A1-A and butyryl coenzyme A synthetase
PT   expression levels.
XX
PS   Claim 1; SEQ ID NO 1; 126pp; Japanese.
XX
CC   The invention comprises a method for detecting prostatic cancer in a
CC   subject. The method involves measuring the expression levels of specific
CC   genes: transient receptor potential cation channel, subfamily M, member 4
CC   (TRPM4); phospholipase A1-A (PLA1A); and butyryl coenzyme A synthetase 1
CC   (BUCS1). The method of the invention is useful for the detection and
CC   treatment of prostate cancer. The present cDNA sequence encodes the human
CC   TRPM4b protein of the invention.
XX
SQ   Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;
```

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  Query Match           100.0%;  Score 3642;  DB 13;  Length 4061;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3642;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAGAAGAAGACCTGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 ATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAGAAGAAGACCTGC 132

Qy         61 ACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAGTGTGGGCGCCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 ACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAGTGTGGGCGCCCC 192

Qy        121 CGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCCGTGGTGACCGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 CGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCCGTGGTGACCGTG 252

Qy        181 TGGGACAGCGATGCACACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 TGGGACAGCGATGCACACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTC 312

Qy        241 ACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 ACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCT 372

Qy        301 GCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 GCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCA 432

Qy        361 GTGCTGGGGGGGATCGGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 GTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGT 492

Qy        421 GGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 GGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACG 552

Qy        481 GGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 GGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGC 612

Qy        541 ACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 ACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTC 672

Qy        601 ATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 ATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGG 732

Qy        661 GTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 GTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACAC 792

Qy        721 GGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 GGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAG 852
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Qy       781 AAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGT 840
Db       853 AAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGT 912

Qy       841 GATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTC 900
Db       913 GATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTC 972

Qy       901 GTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCC 960
Db       973 GTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCC 1032

Qy       961 CCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCC 1020
Db      1033 CCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCC 1092

Qy      1021 AAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTC 1080
Db      1093 AAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTC 1152

Qy      1081 CTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCC 1140
Db      1153 CTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCC 1212

Qy      1141 CTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCT 1200
Db      1213 CTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCT 1272

Qy      1201 GTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGG 1260
Db      1273 GTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGG 1332

Qy      1261 CGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTC 1320
Db      1333 CGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTC 1392

Qy      1321 GTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTG 1380
Db      1393 GTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTG 1452

Qy      1381 GCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCG 1440
Db      1453 GCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCG 1512

Qy      1441 TCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCC 1500
Db      1513 TCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCC 1572

Qy      1501 CCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCC 1560
Db      1573 CCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCC 1632

Qy      1561 TCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTC 1620
Db      1633 TCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTC 1692

Qy      1621 TCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGC 1680
Db      1693 TCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGC 1752

Qy      1681 GACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAG 1740
Db      1753 GACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAG 1812

Qy      1741 ATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCA 1800
Db      1813 ATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCA 1872

Qy      1801 CGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAG 1860
Db      1873 CGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAG 1932

Qy      1861 GGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGC 1920
Db      1933 GGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGC 1992

Qy      1921 CTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAA 1980
Db      1993 CTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAA 2052

Qy      1981 GCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGG 2040
Db      2053 GCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGG 2112

Qy      2041 TGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCT 2100
Db      2113 TGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCT 2172

Qy      2101 CCACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAG 2160
Db      2173 CCACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAG 2232

Qy      2161 GAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGAC 2220
Db      2233 GAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGAC 2292

Qy      2221 CCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGG 2280
Db      2293 CCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGG 2352

Qy      2281 GGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTG 2340
Db      2353 GGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTG 2412

Qy      2341 ACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTG 2400
Db      2413 ACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTG 2472

Qy      2401 CTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGG 2460
Db      2473 CTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGG 2532

Qy      2461 GCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTC 2520
Db      2533 GCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTC 2592

Qy      2521 GCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTC 2580
Db      2593 GCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTC 2652

Qy      2581 GCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGC 2640
Db      2653 GCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGC 2712

Qy      2641 TGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATG 2700
Db      2713 TGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATG 2772

Qy      2701 GTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATC 2760
Db      2773 GTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATC 2832

Qy      2761 GTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGG 2820
Db      2833 GTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGG 2892

Qy      2821 CTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCA 2880
Db      2893 CTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCA 2952

Qy      2881 AGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAG 2940
Db      2953 AGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAG 3012

Qy      2941 GAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGG 3000
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Db       3013 GAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGG 3072

Qy       3001 GCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3073 GCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTG 3132

Qy       3061 GTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATT 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3133 GTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATT 3192

Qy       3121 GCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCG 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3193 GCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCG 3252

Qy       3181 CAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATC 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3253 CAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATC 3312

Qy       3241 GTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAG 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3313 GTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAG 3372

Qy       3301 CCGTCCTCCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAG 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3373 CCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAG 3432

Qy       3361 CTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3433 CTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAG 3492

Qy       3421 CGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAA 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3493 CGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAA 3552

Qy       3481 CAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAG 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3553 CAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAG 3612

Qy       3541 CAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCC 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3613 CAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCC 3672

Qy       3601 CCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGAC 3642
             |||||||||||||||||||||||||||||||||||||||||||
Db       3673 CCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGAC 3714


RESULT 5
AAD32372
ID   AAD32372 standard; cDNA; 4042 BP.
XX
AC   AAD32372;
XX
DT   18-JUN-2002 (first entry)
XX
DE   Human Trp9 protein encoding cDNA.
XX
KW   Human; prostate carcinoma associated protein; Trp9; Trp10a; Trp10b;
KW   transient receptor potential; calcium channel protein; Trp8a; Trp8b;
KW   molecular marker; endometrial cancer; uterine carcinoma; melanoma; gene;
KW   tumour; chorion carcinoma; lung cancer; antisense therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             42. .3686
FT                   /*tag= a
FT                   /product= "Human Trp9 protein"
XX
PN   WO200210382-A2.
XX
PD   07-FEB-2002.
XX
PF   18-JUL-2001; 2001WO-EP008309.
XX
PR   28-JUL-2000; 2000US-0221513P.
XX
PA   (WISS/) WISSENBACH U.
XX
PI   Wissenbach U;
XX
DR   WPI; 2002-269013/31.
DR   P-PSDB; AAE20283.
XX
PT   Novel isolated nucleic acid encoding human prostate carcinoma associated
PT   protein such as transient receptor potential 8a, 8b, 10a, 10b proteins,
PT   useful as molecular markers for diagnosing prostate cancer.
XX
PS   Claim 1; Fig 9A; 70pp; English.
XX
CC   The invention relates to human prostate carcinoma associated proteins
CC   such as transient receptor potential (Trp)8a, Trp8b, Trp9, Trp10a and
CC   Trp10b and nucleic acid molecules encoding such polypeptides. Trp8, Trp9,
CC   Trp10 are novel calcium channel proteins. Sequences of the invention are
CC   useful as molecular markers for diagnosing prostate cancer. Sequences of
CC   the invention, their antibodies, inhibitors and antisense molecules are
CC   useful for preventing, treating or ameliorating a prostate tumour,
CC   endometrial cancer (uterine carcinoma), tumour, a chorion carcinoma,
CC   cancer of the lung or melanoma. Polynucleotides of the invention are used
CC   in antisense therapy. The present sequence is human Trp9 protein encoding
CC   cDNA
XX
SQ   Sequence 4042 BP; 703 A; 1260 C; 1290 G; 789 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 3640.4;  DB 6;  Length 4042;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3641;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAGAAGAAGACCTGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         42 ATGGTGGTGCCGGAGAAGGAGCAGAGCTGGATCCCCAAGATCTTCAAGAAGAAGACCTGC 101

Qy         61 ACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAGTGTGGGCGCCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 ACGACGTTCATAGTTGACTCCACAGATCCGGGAGGGACCTTGTGCCAGTGTGGGCGCCCC 161

Qy        121 CGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCCGTGGTGACCGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 CGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCCGTGGTGACCGTG 221

Qy        181 TGGGACAGCGATGCACACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 TGGGACAGCGATGCACACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTC 281

Qy        241 ACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 ACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCT 341

Qy        301 GCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 GCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCA 401

Qy        361 GTGCTGGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 GTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGT 461

Qy        421 GGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 GGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACG 521

Qy        481 GGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 GGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGC 581

Qy        541 ACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       582 ACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTC 641
Qy       601 ATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGG 660
Db       642 ATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGG 701
Qy       661 GTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACAC 720
Db       702 GTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACAC 761
Qy       721 GGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAG 780
Db       762 GGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAG 821
Qy       781 AAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGT 840
Db       822 AAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGT 881
Qy       841 GATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTC 900
Db       882 GATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTC 941
Qy       901 GTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCC 960
Db       942 GTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCC 1001
Qy       961 CCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCC 1020
Db      1002 CCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCC 1061
Qy       1021 AAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTC 1080
Db      1062 AAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTC 1121
Qy       1081 CTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCC 1140
Db      1122 CTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCC 1181
Qy       1141 CTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCT 1200
Db      1182 CTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCT 1241
Qy       1201 GTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGG 1260
Db      1242 GTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGG 1301
Qy       1261 CGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTC 1320
Db      1302 CGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTC 1361
Qy       1321 GTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTG 1380
Db      1362 GTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTG 1421
Qy       1381 GCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCG 1440
Db      1422 GCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCG 1481
Qy       1441 TCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCC 1500
Db      1482 TCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCC 1541
Qy       1501 CCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCC 1560
Db      1542 CCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCC 1601
Qy       1561 TCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTC 1620
Db      1602 TCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTC 1661
Qy       1621 TCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGC 1680
Db      1662 TCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGC 1721

Qy       1681 GACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAG 1740
Db      1722 GACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAG 1781
Qy       1741 ATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCA 1800
Db      1782 ATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCA 1841
Qy       1801 CGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAG 1860
Db      1842 CGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAG 1901
Qy       1861 GGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGC 1920
Db      1902 GGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGC 1961
Qy       1921 CTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAA 1980
Db      1962 CTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAA 2021
Qy       1981 GCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGG 2040
Db      2022 GCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGG 2081
Qy       2041 TGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCT 2100
Db      2082 TGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCT 2141
Qy       2101 CCACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAG 2160
Db      2142 CCACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAG 2201
Qy       2161 GAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGAC 2220
Db      2202 GAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGAC 2261
Qy       2221 CCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGG 2280
Db      2262 CCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGG 2321
Qy       2281 GGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTG 2340
Db      2322 GGCCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGTGCCGGTG 2381
Qy       2341 ACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTG 2400
Db      2382 ACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTG 2441
Qy       2401 CTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGG 2460
Db      2442 CTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGG 2501
Qy       2461 GCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTC 2520
Db      2502 GCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTC 2561
Qy       2521 GCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTC 2580
Db      2562 GCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTC 2621
Qy       2581 GCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGC 2640
Db      2622 GCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGC 2681
Qy       2641 TGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATG 2700
Db      2682 TGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATG 2741
Qy       2701 GTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATC 2760
Db      2742 GTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATC 2801
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Qy       2761 GTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGG 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2802 GTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGG 2861

Qy       2821 CTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCA 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2862 CTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCA 2921

Qy       2881 AGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAG 2940
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Db       2922 AGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAG 2981

Qy       2941 GAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2982 GAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGG 3041

Qy       3001 GCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3061 GTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATT 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3102 GTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATT 3161

Qy       3121 GCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCG 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3162 GCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCG 3221

Qy       3181 CAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATC 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3222 CAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATC 3281

Qy       3241 GTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAG 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3282 GTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAG 3341

Qy       3301 CCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAG 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3342 CCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAG 3401

Qy       3361 CTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3402 CTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAG 3461

Qy       3421 CGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAA 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3462 CGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAA 3521

Qy       3481 CAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAG 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3522 CAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAG 3581

Qy       3541 CAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCC 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3582 CAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCC 3641

Qy       3601 CCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGAC 3642
             |||||||||||||||||||||||||||||||||||||||||||
Db       3642 CCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGAC 3683
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RESULT 6
ABK92224
ID ABK92224 standard; DNA; 3501 BP.
XX
AC ABK92224;
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated DNA sequence #110.
XX
KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.
XX
OS Mammalia.
XX
PN WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032045.
XX
PR 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-0263957P.
PR 16-MAR-2001; 2001US-0276791P.
PR 16-MAR-2001; 2001US-0276888P.
PR 06-APR-2001; 2001US-0281922P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0288589P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Gish KC, Mack DH, Wilson KE; Afar D, Hevezi P;
XX
DR WPI; 2002-471335/50.
DR P-PSDB; ABG61907.
XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
XX
PS Claim 22; Page 390-391; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridise to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX
SQ Sequence 3501 BP; 579 A; 1094 C; 1131 G; 697 T; 0 U; 0 Other;

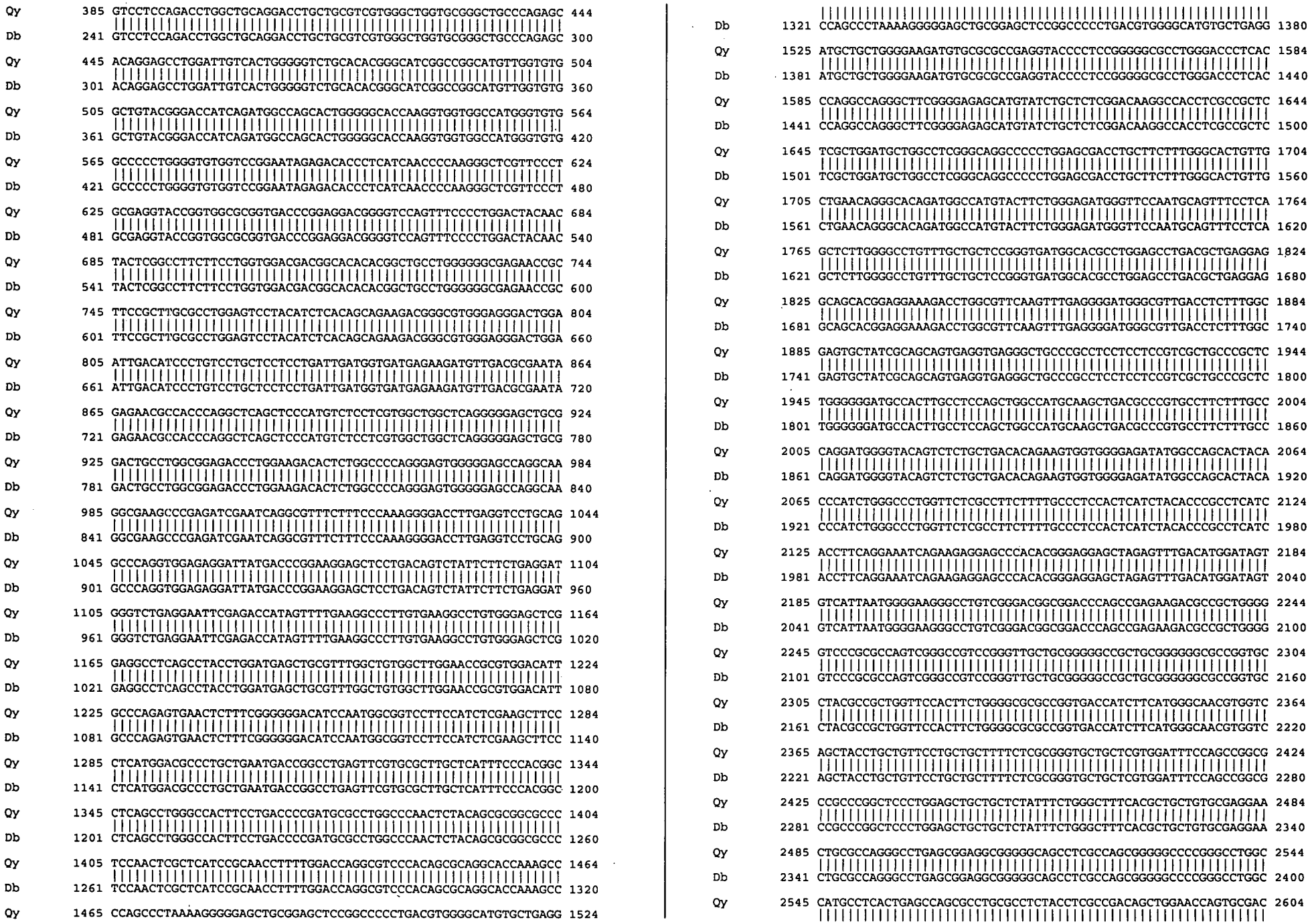
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  Query Match             96.0%;  Score 3498;  DB 6;  Length 3501;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3498;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        145 ATGGAGGATGCCTTCGGGGCAGCCGTGGTGACCGTGTGGGACAGCGATGCACACACCACG 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGGATGCCTTCGGGGCAGCCGTGGTGACCGTGTGGGACAGCGATGCACACACCACG 60

Qy        205 GAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGCACAGC 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGCACAGC 120

Qy        265 AATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCACACGC 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCACACGC 180

Qy        325 ACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGGGCCCC 384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGGGCCCC 240
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Qy 385 GTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCCAGAGC 444
Db 241 GTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCCAGAGC 300
Qy 445 ACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTGGTGTG 504
Db 301 ACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTGGTGTG 360
Qy 505 GCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGGGTGTG 564
Db 361 GCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGGGTGTG 420
Qy 565 GCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGTTCCCT 624
Db 421 GCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGTTCCCT 480
Qy 625 GCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACTACAAC 684
Db 481 GCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACTACAAC 540
Qy 685 TACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGAACCGC 744
Db 541 TACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGAACCGC 600
Qy 745 TTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGACTGGA 804
Db 601 TTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGACTGGA 660
Qy 805 ATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGCGAATA 864
Db 661 ATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGCGAATA 720
Qy 865 GAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAGCTGCG 924
Db 721 GAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAGCTGCG 780
Qy 925 GACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCAGGCAA 984
Db 781 GACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCAGGCAA 840
Qy 985 GGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCCTGCAG 1044
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Qy 1045 GCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTGAGGAT 1104
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Qy 1105 GGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGAGCTCG 1164
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Db 1021 GAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGGACATT 1080
Qy 1225 GCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAGCTTCC 1284
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Db 1141 CTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGC 1200
Qy 1345 CTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCC 1404
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Db 1261 TCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCC 1320
Qy 1465 CCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGG 1524
Db 1321 CCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGG 1380
Qy 1525 ATGCTGCTGGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCAC 1584
Db 1381 ATGCTGCTGGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCAC 1440
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Db 1441 CCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTC 1500
Qy 1645 TCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTG 1704
Db 1501 TCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTG 1560
Qy 1705 CTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCA 1764
Db 1561 CTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCA 1620
Qy 1765 GCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAG 1824
Db 1621 GCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAG 1680
Qy 1825 GCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGC 1884
Db 1681 GCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGC 1740
Qy 1885 GAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTC 1944
Db 1741 GAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTC 1800
Qy 1945 TGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCC 2004
Db 1801 TGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCC 1860
Qy 2005 CAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACA 2064
Db 1861 CAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACA 1920
Qy 2065 CCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATC 2124
Db 1921 CCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATC 1980
Qy 2125 ACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGT 2184
Db 1981 ACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGT 2040
Qy 2185 GTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGG 2244
Db 2041 GTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGG 2100
Qy 2245 GTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGC 2304
Db 2101 GTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGC 2160
Qy 2305 CTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTC 2364
Db 2161 CTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTC 2220
Qy 2365 AGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCG 2424
Db 2221 AGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCG 2280
Qy 2425 CCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAA 2484
Db 2281 CCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAA 2340
Qy 2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
Db 2341 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2400
Qy 2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
Db

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Db       2401 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2460

Qy       2605 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2664
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Db       2461 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2520

Qy       2665 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2724
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2580

Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2640

Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
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Db       2641 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2700

Qy       2845 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2904
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2760

Qy       2905 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2964
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2820

Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 2880

Qy       3025 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3084
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 2940

Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
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Db       2941 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3000

Qy       3145 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3204
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Db       3001 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3060

Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
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Db       3061 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3120

Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
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Db       3121 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3180

Qy       3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3384
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Db       3181 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3240

Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
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Db       3241 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3300

Qy       3445 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3504
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3360

Qy       3505 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3564
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3420

Qy       3565 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3624
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3480

Qy       3625 CTGCCTGGGTCCAAAGAC 3642
             ||||||||||||||||||
Db       3481 CTGCCTGGGTCCAAAGAC 3498
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RESULT 7
ADN39597
ID   ADN39597 standard; cDNA; 3501 BP.
XX
AC   ADN39597;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:A197.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003042661-A2.
XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036810.
XX
PR   13-NOV-2001; 2001US-0350666P.
PR   21-NOV-2001; 2001US-0332464P.
PR   29-NOV-2001; 2001US-0334393P.
PR   03-DEC-2001; 2001US-0335394P.
PR   14-DEC-2001; 2001US-0340376P.
PR   08-JAN-2002; 2002US-0347211P.
PR   10-JAN-2002; 2002US-0347349P.
PR   08-FEB-2002; 2002US-0355250P.
PR   13-FEB-2002; 2002US-0356714P.
PR   20-FEB-2002; 2002US-0359077P.
PR   29-MAR-2002; 2002US-0368809P.
PR   04-APR-2002; 2002US-0370110P.
PR   12-APR-2002; 2002US-0372246P.
PR   05-JUN-2002; 2002US-0386614P.
PR   16-JUL-2002; 2002US-0396839P.
PR   22-JUL-2002; 2002US-0397775P.
PR   22-JUL-2002; 2002US-0397845P.
PR   09-SEP-2002; 2002US-0409450P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D,  Aziz N,  Ginsburg WM,  Gish KC,  Glynne R,  Hevezi PA;
PI   Mack DH,  Murray R,  Watson SR,  Wilson KE,  Zlotnik A;
XX
DR   WPI; 2003-468649/44.
DR   P-PSDB; ADN39598.
XX
PT   Determining the presence or absence of a pathological cell in a patient,
PT   useful for diagnosing, prognosing or treating cancer, comprises detecting
PT   a nucleic acid in a biological sample.
XX
PS   Claim 8; SEQ ID NO A197; 1385pp; English.
XX
CC   The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC   whose expression is upregulated or downregulated in specific cancers or
CC   other diseases such as angiogenic or fibrotic disorders, and to methods
CC   of determining the presence or absence of a pathological cell in a
CC   patient by detecting a nucleic acid at least 80% identical to those of
CC   the invention or by detecting a polypeptide of the invention. The
CC   invention also relates to expression vectors and host cells comprising a
CC   nucleic acid of the invention; antibodies which specifically bind a
CC   polypeptide of the invention; use of such antibodies for drug targeting;
CC   and methods of screening for modulators of activity or expression of the
CC   polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC   antibodies and methods are useful for diagnosing, prognosing and treating
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CC   cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC   atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC   neovascularistaion syndromes, scarring and uterine fibroids. They may
CC   also be useful in wound healing and in contraception. The present
CC   sequence represents a nucleic acid sequence of the invention.
XX
SQ   Sequence 3501 BP; 579 A; 1094 C; 1131 G; 697 T; 0 U; 0 Other;

  Query Match             96.0%;  Score 3498;  DB 11;  Length 3501;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3498;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        145 ATGGAGGATGCCTTCGGGGCAGCCGTGGTGACCGTGTGGGACAGCGATGCACACACCACG 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGGATGCCTTCGGGGCAGCCGTGGTGACCGTGTGGGACAGCGATGCACACACCACG 60

Qy        205 GAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGCACAGC 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGCACAGC 120

Qy        265 AATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCACACGC 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCACACGC 180

Qy        325 ACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGGGCCCC 384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGGGCCCC 240

Qy        385 GTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCCAGAGC 444
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCCAGAGC 300

Qy        445 ACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTGGTGTG 504
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Qy        505 GCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGGGTGTG 564
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGGGTGTG 420

Qy        565 GCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGTTCCCT 624
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGTTCCCT 480

Qy        625 GCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACTACAAC 684
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACTACAAC 540

Qy        685 TACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGAACCGC 744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGAACCGC 600

Qy        745 TTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGACTGGA 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGACTGGA 660

Qy        805 ATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGCGAATA 864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGCGAATA 720

Qy        865 GAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAGCTGCG 924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAGCTGCG 780

Qy        925 GACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCAGGCAA 984
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCAGGCAA 840

Qy        985 GGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCCTGCAG 1044
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Db        841 GGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCCTGCAG 900

Qy       1045 GCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTGAGGAT 1104
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Db        901 GCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTGAGGAT 960

Qy       1105 GGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGAGCTCG 1164
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Db        961 GGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGAGCTCG 1020

Qy       1165 GAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGGACATT 1224
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Db       1021 GAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGGACATT 1080

Qy       1225 GCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAGCTTCC 1284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAGCTTCC 1140

Qy       1285 CTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGC 1344
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Db       1141 CTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGC 1200

Qy       1345 CTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCC 1404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCC 1260

Qy       1405 TCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCC 1464
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Db       1261 TCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCC 1320

Qy       1465 CCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGG 1524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGG 1380

Qy       1525 ATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCAC 1584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCAC 1440

Qy       1585 CCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTC 1644
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Db       1441 CCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTC 1500

Qy       1645 TCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTG 1704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTG 1560

Qy       1705 CTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCA 1764
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Db       1561 CTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCA 1620

Qy       1765 GCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAG 1824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAG 1680

Qy       1825 GCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGC 1884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGC 1740

Qy       1885 GAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTC 1944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTC 1800

Qy       1945 TGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCC 2004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCC 1860

Qy       2005 CAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACA 2064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACA 1920

Qy       2065 CCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATC 2124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATC 1980

Qy       2125 ACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGT 2184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1981 ACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGT 2040
Qy       2185 GTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGG 2244
Db       2041 GTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGG 2100
Qy       2245 GTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGC 2304
Db       2101 GTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGC 2160
Qy       2305 CTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTC 2364
Db       2161 CTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTC 2220
Qy       2365 AGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCG 2424
Db       2221 AGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCG 2280
Qy       2425 CCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAA 2484
Db       2281 CCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAA 2340
Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
Db       2341 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2400
Qy       2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
Db       2401 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2460
Qy       2605 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2664
Db       2461 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2520
Qy       2665 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2724
Db       2521 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2580
Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
Db       2581 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2640
Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
Db       2641 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2700
Qy       2845 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2904
Db       2701 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2760
Qy       2905 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2964
Db       2761 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2820
Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
Db       2821 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 2880
Qy       3025 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3084
Db       2881 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 2940
Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
Db       2941 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3000
Qy       3145 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3204
Db       3001 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3060
Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
Db       3061 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3120
Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
Db       3121 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3180
Qy       3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3384
Db       3181 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3240
Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
Db       3241 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3300
Qy       3445 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3504
Db       3301 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3360
Qy       3505 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3564
Db       3361 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3420
Qy       3565 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3624
Db       3421 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3480
Qy       3625 CTGCCTGGGTCCAAAGAC 3642
Db       3481 CTGCCTGGGTCCAAAGAC 3498
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RESULT 8
ADN39239
ID ADN39239 standard; cDNA; 4641 BP.
XX
AC ADN39239;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:557.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnerary; gene therapy; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003042661-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.

PR 09-SEP-2002; 2002US-0409450P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR WPI; 2003-468649/44.
DR P-PSDB; ADN39240.
XX
PT Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
PS Claim 8; SEQ ID NO 557; 1385pp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularistaion syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.
XX
SQ Sequence 4641 BP; 808 A; 1459 C; 1432 G; 942 T; 0 U; 0 Other;

Query Match 96.0%; Score 3498; DB 11; Length 4641;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       145 ATGGAGGATGCCTTCGGGGCAGCCGTGGTGACCGTGTGGGACAGCGATGCACACACCACG 204
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Db       769 ATGGAGGATGCCTTCGGGGCAGCCGTGGTGACCGTGTGGGACAGCGATGCACACACCACG 828

Qy       205 GAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGCACAGC 264
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       829 GAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGCACAGC 888

Qy       265 AATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCACACGC 324
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       889 AATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCACACGC 948

Qy       325 ACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGGGCCCC 384
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       949 ACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGGGCCCC 1008

Qy       385 GTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCCAGAGC 444
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1009 GTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCCAGAGC 1068

Qy       445 ACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTGGTGTG 504
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1069 ACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTGGTGTG 1128

Qy       505 GCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGGGTGTG 564
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1129 GCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGGGTGTG 1188

Qy       565 GCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGTTCCCT 624
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Db      1189 GCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGTTCCCT 1248

Qy       625 GCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACTACAAC 684
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Db      1249 GCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACTACAAC 1308

Qy       685 TACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGAACCGC 744
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1309 TACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGAACCGC 1368

Qy       745 TTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGACTGGA 804
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1369 TTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGACTGGA 1428

Qy       805 ATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGCGAATA 864
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1429 ATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGCGAATA 1488

Qy       865 GAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAGCTGCG 924
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1489 GAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAGCTGCG 1548

Qy       925 GACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCAGGCAA 984
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1549 GACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCAGGCAA 1608

Qy       985 GGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCCTGCAG 1044
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Db      1609 GGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCCTGCAG 1668

Qy      1045 GCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTGAGGAT 1104
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Db      1669 GCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTGAGGAT 1728

Qy      1105 GGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGAGCTCG 1164
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Db      1729 GGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGAGCTCG 1788

Qy      1165 GAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGGACATT 1224
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Db      1789 GAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGGACATT 1848

Qy      1225 GCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAGCTTCC 1284
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1849 GCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAGCTTCC 1908

Qy      1285 CTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGC 1344
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1909 CTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGC 1968

Qy      1345 CTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCC 1404
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Db      1969 CTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCC 2028

Qy      1405 TCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCC 1464
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2029 TCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCC 2088

Qy      1465 CCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGG 1524
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2089 CCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTGAGG 2148

Qy      1525 ATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCAC 1584
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Db      2149 ATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCAC 2208

Qy      1585 CCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTC 1644
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Db      2209 CCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTC 2268

Qy      1645 TCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTG 1704
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2269 TCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTG 2328

Qy      1705 CTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCA 1764
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Db       2329 CTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCCTCA 2388

Qy       1765 GCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAG 1824
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Db       2389 GCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAG 2448

Qy       1825 GCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGC 1884
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2449 GCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGC 2508

Qy       1885 GAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTC 1944
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2509 GAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCCCGCTC 2568

Qy       1945 TGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCC 2004
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2569 TGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCTTTGCC 2628

Qy       2005 CAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACA 2064
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2629 CAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACTACA 2688

Qy       2065 CCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATC 2124
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Db       2689 CCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATC 2748

Qy       2125 ACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGT 2184
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Db       2749 ACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGGATAGT 2808

Qy       2185 GTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGG 2244
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2809 GTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGG 2868

Qy       2245 GTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCCGGTGC 2304
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Db       2869 GTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGCGCCGGTGC 2928

Qy       2305 CTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTC 2364
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Db       2929 CTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTGGTC 2988

Qy       2365 AGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCG 2424
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Db       2989 AGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGCCGGCG 3048

Qy       2425 CCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAA 2484
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Db       3049 CCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAA 3108

Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
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Db       3109 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 3168

Qy       2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3169 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 3228

Qy       2605 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2664
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Db       3229 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 3288

Qy       2665 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2724
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Db       3289 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 3348

Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
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Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
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Db       3409 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 3468

Qy       2845 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2904
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Db       3469 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 3528

Qy       2905 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2964
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Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
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Db       3589 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3648

Qy       3025 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3084
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Db       3649 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3708

Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
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Db       3709 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3768

Qy       3145 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3204
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Db       3769 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3828

Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
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Db       3829 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3888

Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
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Db       3889 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3948

Qy       3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3384
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Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
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Qy       3445 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3504
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Db       4069 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 4128

Qy       3505 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3564
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Db       4129 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 4188

Qy       3565 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3624
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Db       4189 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 4248

Qy       3625 CTGCCTGGGTCCAAAGAC 3642
             ||||||||||||||||||
Db       4249 CTGCCTGGGTCCAAAGAC 4266
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RESULT 9
ADL06463
ID   ADL06463 standard; cDNA; 3898 BP.
XX
AC   ADL06463;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human tumour-associated antigenic target (TAT) cDNA sequence #43.
XX
KW   Human; tumour-associated antigenic target; TAT; cell death; tumour;
KW   cancer; cytostatic; gene; ss.
XX
OS   Homo sapiens.
XX
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PN WO2004016225-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US025892.
XX
PR 19-AUG-2002; 2002US-0404809P.
PR 21-AUG-2002; 2002US-0405645P.
PR 23-SEP-2002; 2002US-0413192P.
PR 15-OCT-2002; 2002US-0419008P.
PR 15-NOV-2002; 2002US-0426847P.
PR 02-JUL-2003; 2003US-0484959P.
XX
PA (GETH) GENENTECH INC.
XX
PI Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;
PI Spencer SD, Wu TD, Zhang Z;
XX
DR WPI; 2004-257144/24.
DR P-PSDB; ADL06543.
XX
PT New antibody that binds to a tumor-associated antigenic target (TAT)
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating cancer.
XX
PS Claim 1; SEQ ID NO 43; 319pp; English.
XX
CC The present invention relates to the isolation of human tumour-associated
CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
CC produced in bacteria or in CHO cells and induces death of a cell to which
CC it binds. The antibody is useful for preparing a composition for
CC diagnosing or treating tumours and cancer. The present sequence
CC represents a human TAT cDNA sequence of the invention.
XX
SQ Sequence 3898 BP; 685 A; 1207 C; 1235 G; 771 T; 0 U; 0 Other;

Query Match 95.4%; Score 3473.8; DB 12; Length 3898;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3506; Conservative 0; Mismatches 17; Indels 2; Gaps 2;

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Qy        118 CCCCGGACCGCCCACCCCGCAGTGGCCATGGAGGATGCCTTCGGGGCAGCCGTGGTGACC 177
              |||| |  |||||||||||||||||||||||| || ||||||||||||||||||||||||
Db          7 CCCCCGGACGCCCACCCCGCAGTGGCCATGGA-GAAGCCTTCGGGGCAGCCGTGGTGACC 65

Qy        178 GTGTGGGACAGCGATGCAC-ACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGA 236
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         66 GTGTGGGACAGCGATGCACAACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGA 125

Qy        237 CTTCACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCC 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CTTCACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCC 185

Qy        297 AGCTGCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGT 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AGCTGCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGT 245

Qy        357 GTCAGTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCG 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GTCAGTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCG 305

Qy        417 TCGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCA 476
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TCGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCA 365

Qy        477 CACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGG 536
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGG 425

Qy        537 GGGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACAC 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GGGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACAC 485

Qy        597 CCTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGA 656
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CCTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGA 545

Qy        657 CGGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCAC 716
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CGGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCAC 605

Qy        717 ACACGGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACA 776
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 ACACGGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACA 665

Qy        777 GCAGAAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGA 836
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 GCAGAAGACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGA 725

Qy        837 TGGTGATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCT 896
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TGGTGATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCT 785

Qy        897 CCTCGTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCT 956
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 CCTCGTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCT 845

Qy        957 GGCCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTT 1016
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 GGCCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTT 905

Qy       1017 TCCCAAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGA 1076
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Db        906 TCCCAAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGA 965

Qy       1077 GCTCCTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAA 1136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GCTCCTGACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAA 1025

Qy       1137 GGCCCTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTT 1196
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Db       1026 GGCCCTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTT 1085

Qy       1197 GGCTGTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCA 1256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1086 GGCTGTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCA 1145

Qy       1257 ATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGA 1316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 ATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGA 1205

Qy       1317 GTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCG 1376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1206 GTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCG 1265

Qy       1377 CCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCA 1436
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Db       1266 CCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCA 1325

Qy       1437 GGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCG 1496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 GGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCG 1385

Qy       1497 GCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTA 1556
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1386 GCCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTA 1445

Qy       1557 CCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCT 1616
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1446 CCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCT 1505

Qy       1617 GCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTG 1676
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1506 GCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTG 1565
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Qy      1677 GAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTG 1736
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Qy      1737 GGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGAT 1796
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Db      1626 GGAGATGGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGAT 1685

Qy      1797 GGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTT 1856
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1686 GGCACGCCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTT 1745

Qy      1857 TGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGC 1916
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Db      1746 TGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGC 1805

Qy      1917 CCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCAT 1976
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1806 CCGCCTCCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCAT 1865

Qy      1977 GCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAA 2036
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1866 GCAAGCTGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAA 1925

Qy      2037 GTGGTGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTG 2096
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Db      1926 GTGGTGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTG 1985

Qy      2097 CCCTCCACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACG 2156
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1986 CCCTCCACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACG 2045

Qy      2157 GGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGC 2216
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Db      2046 GGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGC 2105

Qy      2217 GGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTG 2276
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2106 GGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTG 2165

Qy      2277 CGGGGGCCGCTGCGGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCC 2336
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Db      2166 CGGGGGCCGCTGCGGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCC 2225

Qy      2337 GGTGACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCG 2396
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2226 GGTGACCATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCTTGCTGCTTTTCTCGCG 2285

Qy      2397 GGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTT 2456
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2286 GGTGCTGCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTT 2345

Qy      2457 CTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAG 2516
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Db      2346 CTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAG 2405

Qy      2517 CCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTA 2576
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2406 CCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTA 2465

Qy      2577 CCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGT 2636
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2466 CCTCGCCGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGT 2525

Qy      2637 GGGCTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTT 2696
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2526 GGGCTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTT 2585

Qy      2697 CATGGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAA 2756
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2586 CATGGTTTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAA 2645

Qy      2757 GATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGT 2816
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Db      2646 GATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGT 2705

Qy      2817 GTGGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTT 2876
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Db      2706 GTGGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTT 2765

Qy      2877 CCCAAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCC 2936
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Db      2766 CCCAAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCC 2825

Qy      2937 CCAGGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTT 2996
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Db      2826 CCAGGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTT 2885

Qy      2997 CTGGGCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCT 3056
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Qy      3057 GGTGGTGCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCT 3116
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Qy      3117 CATTGCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAA 3176
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Db      3006 CATTGCCATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAA 3065

Qy      3177 GGCGCAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTT 3236
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3066 GGCGCAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTT 3125

Qy      3237 TATCGTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCC 3296
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3126 TATCGTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCC 3185

Qy      3297 CCAGCCGTCCTCCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCG 3356
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3186 CCAGCCGTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCG 3245

Qy      3357 GAAGCTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGA 3416
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3246 GAAGCTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGA 3305

Qy      3417 CAAGCGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACT 3476
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db      3306 CAAGCGGGAGAGCGACTCCGAGCGTCTGGAGCGCACGTCCCAGAAGGTGGACTTGGCACT 3365

Qy      3477 GAAACAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGT 3536
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3366 GAAACAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGT 3425

Qy      3537 CCAGCAGTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCT 3596
             |||||||||||||||||||||||||||||| |  ||||| | ||| |||||||| || |
Db      3426 CCAGCAGTGTAGCCGCGTCCTGGGGTGGGTGACGTAGGCCGTTAGCAGCTCTGCCATGTT 3485

Qy      3597 GCCCCCAGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGA 3641
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Db      3486 GCCCTCAGGTGGGCCGCCACCCCTTGACCTGCATGGGTCCAAAGA 3530
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RESULT 10
ABK92167
ID ABK92167 standard; DNA; 3810 BP.
XX
AC ABK92167;
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated DNA sequence #53.
XX
KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.

XX
OS Mammalia.
XX
PN WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032045.
XX
PR 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-0263957P.
PR 16-MAR-2001; 2001US-0276791P.
PR 16-MAR-2001; 2001US-0276888P.
PR 06-APR-2001; 2001US-0281922P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0288589P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
DR WPI; 2002-471335/50.
DR P-PSDB; ABG61852.
XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
XX
PS Claim 22; Page 339-340; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridise to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX
SQ Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;

Query Match 93.9%; Score 3421.2; DB 6; Length 3810;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3429; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy        200 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 60

Qy        260 ACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCA 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCA 120

Qy        320 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 180

Qy        380 GCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCC 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCC 240

Qy        440 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 499
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Db        241 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 300

Qy        500 GTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGG 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGG 360

Qy        560 GTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGT 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGT 420

Qy        620 TCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACT 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACT 480

Qy        680 ACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGA 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGA 540

Qy        740 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 600

Qy        800 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 660

Qy        860 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 720

Qy        920 CTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCA 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        980 GGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCC 1039
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Db        781 GGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCC 840

Qy       1040 TGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTG 1099
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Qy       1100 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGA 1159
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Db        901 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGA 960

Qy       1160 GCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGG 1219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGG 1020

Qy       1220 ACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAG 1279
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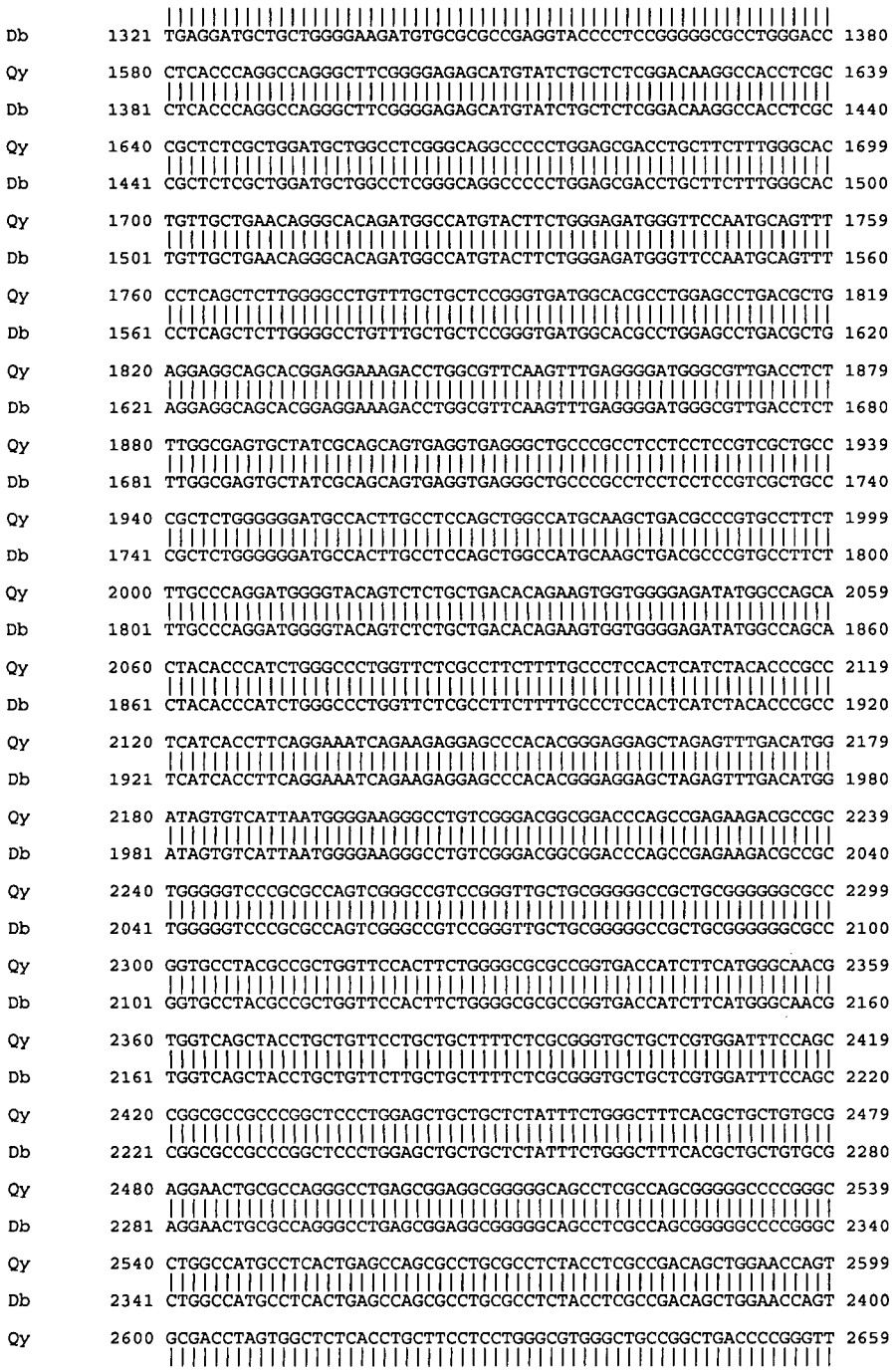
Qy       1280 CTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCC 1339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCC 1140

Qy       1340 ACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGG 1399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGG 1200

Qy       1400 CGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCA 1459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCA 1260

Qy       1460 AAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGC 1519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGC 1320

Qy       1520 TGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGGCGCCTGGGACC 1579
```



RESULT 11
ADR66772

ID ADR66772 standard; DNA; 3810 BP.
XX
AC ADR66772;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived DNA SEQ ID 65 #4.
XX
KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis; ds.
XX
OS Homo sapiens.
XX
PN WO2004076614-A2.
XX
PD 10-SEP-2004.
XX
PF 22-FEB-2004; 2004WO-DE000433.
XX
PR 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemmendorf T, Kinnemann H, Roepcke S;
PI Xinzhong L, Staub E;
XX
DR WPI; 2004-653386/63.
XX
PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
PS Claim 1; Page 1439; 1607pp; German.
XX
CC This invention describes novel cytostatic polynucleotide and polypeptide
CC sequences which can be used in a method for diagnosing prostatic cancer
CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotype, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated
CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.
XX
SQ Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;

Query Match 93.9%; Score 3421.2; DB 13; Length 3810;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3429; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy       200 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 259
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 60

Qy       260 ACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCA 319
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       320 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 379
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 180

Qy       380 GCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCC 439
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCC 240

Qy       440 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 499
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Db       301 GTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGG 360

Qy       560 GTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGT 619
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Qy       620 TCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACT 679
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Db       421 TCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACT 480

Qy       680 ACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGA 739
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 ACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGA 540

Qy       740 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 799
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 600

Qy       800 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 859
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Db       601 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 660

Qy       860 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 919
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 720

Qy       920 CTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCA 979
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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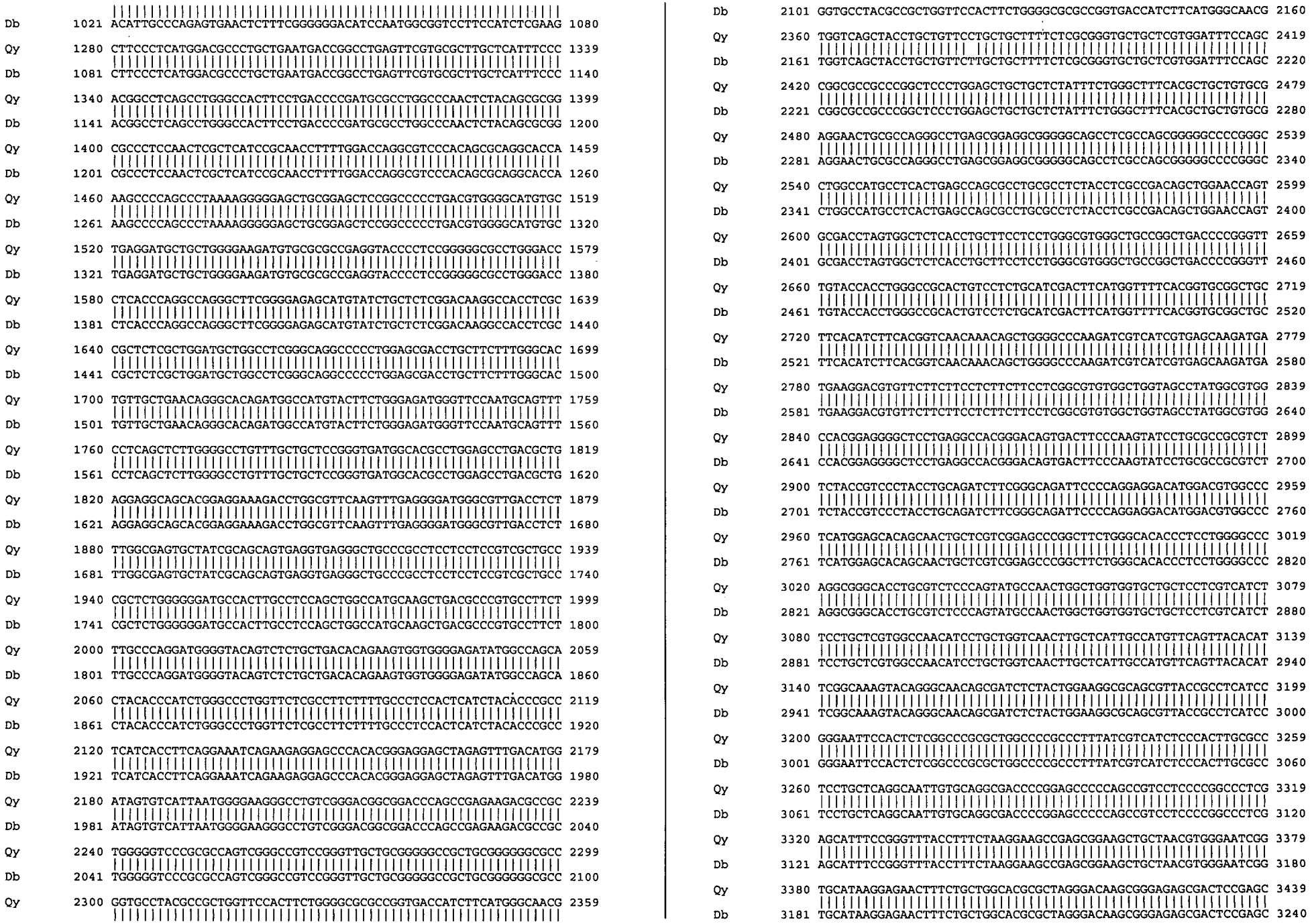
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Qy      1100 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGA 1159
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Db       961 GCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGG 1020

Qy      1220 ACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAG 1279
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Db 1021 ACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAG 1080
Qy 1280 CTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCC 1339
Db 1081 CTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCC 1140
Qy 1340 ACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGG 1399
Db 1141 ACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGG 1200
Qy 1400 CGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCA 1459
Db 1201 CGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCA 1260
Qy 1460 AAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGC 1519
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Qy 1700 TGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTT 1759
Db 1501 TGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTT 1560
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Qy 2360 TGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGC 2419
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Qy 2480 AGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGC 2539
Db 2281 AGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGC 2340
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Qy 2660 TGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGC 2719
Db 2461 TGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGC 2520
Qy 2720 TTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGA 2779
Db 2521 TTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGA 2580
Qy 2780 TGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGG 2839
Db 2581 TGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGG 2640
Qy 2840 CCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCT 2899
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Qy 3020 AGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCT 3079
Db 2821 AGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCT 2880
Qy 3080 TCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACAT 3139
Db 2881 TCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACAT 2940
Qy 3140 TCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCC 3199
Db 2941 TCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCC 3000
Qy 3200 GGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCC 3259
Db 3001 GGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCC 3060
Qy 3260 TCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCG 3319
Db 3061 TCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCG 3120
Qy 3320 AGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGG 3379
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Qy       3440 GTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCG 3499
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Db       3241 GTCTGGAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCG 3300

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Qy       3560 GGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCC 3619
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                |||||||| ||||||||||||
Db       3421 TTGACCTGCATGGGTCCAAAGA 3442
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RESULT 12
ADR65869
ID ADR65869 standard; DNA; 3810 BP.
XX
AC ADR65869;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived DNA SEQ ID 65 #1.
XX
KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis; ds.
XX
OS Homo sapiens.
XX
PN WO2004076614-A2.
XX
PD 10-SEP-2004.
XX
PF 22-FEB-2004; 2004WO-DE000433.
XX
PR 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemmendorf T, Kinnemann H, Roepcke S;
PI Xinzhong L, Staub E;
XX
DR WPI; 2004-653386/63.
XX
PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
PS Claim 1; Page 269; 1607pp; German.
XX
CC This invention describes novel cytostatic polynucleotide and polypeptide
CC sequences which can be used in a method for diagnosing prostatic cancer
CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotype, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated
CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.
XX
SQ Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;

Query Match 93.9%; Score 3421.2; DB 13; Length 3810;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3429; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy        200 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 60

Qy        260 ACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCA 319
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Db         61 ACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCA 120

Qy        320 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 180

Qy        380 GCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCC 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        440 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 300

Qy        500 GTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGG 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGG 360

Qy        560 GTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGT 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGT 420

Qy        620 TCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACT 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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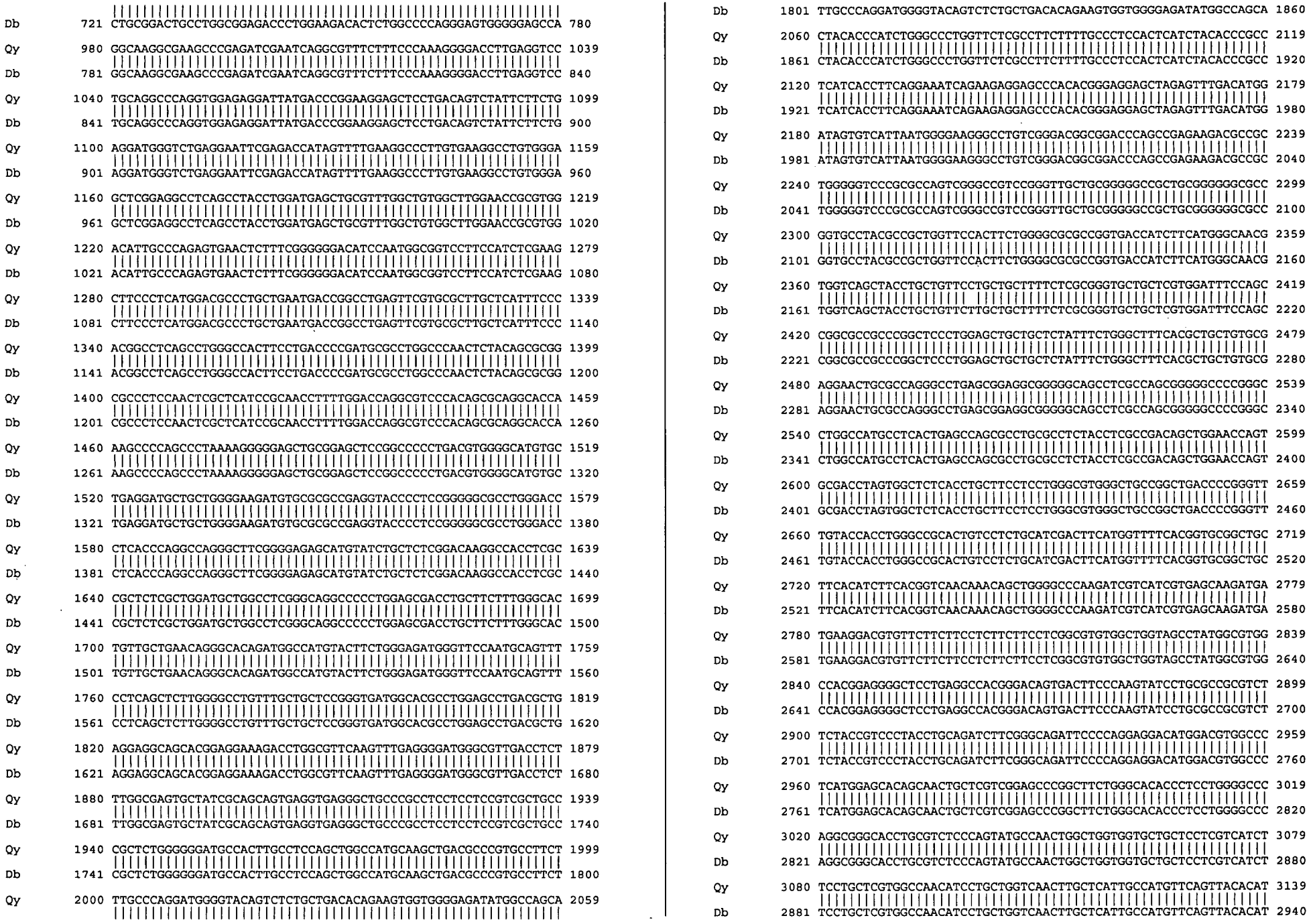
Qy        680 ACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGA 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGA 540

Qy        740 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 600

Qy        800 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 660

Qy        860 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 720

Qy        920 CTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCA 979
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Db 721 CTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCA 780
Qy 980 GGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCC 1039
Db 781 GGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCC 840
Qy 1040 TGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTG 1099
Db 841 TGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTG 900
Qy 1100 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGA 1159
Db 901 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGA 960
Qy 1160 GCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGG 1219
Db 961 GCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGG 1020
Qy 1220 ACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAG 1279
Db 1021 ACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAG 1080
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Db 1141 ACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGG 1200
Qy 1400 CGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCA 1459
Db 1201 CGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCA 1260
Qy 1460 AAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGC 1519
Db 1261 AAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGC 1320
Qy 1520 TGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGGCGCCTGGGACC 1579
Db 1321 TGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACC 1380
Qy 1580 CTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGC 1639
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Qy 1640 CGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCAC 1699
Db 1441 CGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCAC 1500
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Qy 1760 CCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTG 1819
Db 1561 CCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTG 1620
Qy 1820 AGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCT 1879
Db 1621 AGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCT 1680
Qy 1880 TTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCC 1939
Db 1681 TTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCC 1740
Qy 1940 CGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCT 1999
Db 1741 CGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCT 1800
Qy 2000 TTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCA 2059
Db 1801 TTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCA 1860
Qy 2060 CTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCC 2119
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Qy 2180 ATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGC 2239
Db 1981 ATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGC 2040
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Db 2041 TGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCC 2100
Qy 2300 GGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACG 2359
Db 2101 GGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACG 2160
Qy 2360 TGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGC 2419
Db 2161 TGGTCAGCTACCTGCTGTTCTTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGC 2220
Qy 2420 CGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCG 2479
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Qy 2480 AGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGC 2539
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Qy 2540 CTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGT 2599
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Qy 2660 TGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGC 2719
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Qy 2720 TTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGA 2779
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Qy 2840 CCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCT 2899
Db 2641 CCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCT 2700
Qy 2900 TCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCC 2959
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Qy 2960 TCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCC 3019
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Qy       3140 TCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCC 3199
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Qy       3200 GGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCC 3259
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Qy       3260 TCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCG 3319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCG 3120

Qy       3320 AGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGG 3379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 AGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGG 3180

Qy       3380 TGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGC 3439
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Db       3181 TGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGC 3240

Qy       3440 GTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCG 3499
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Qy       3500 AGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGG 3559
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Db       3301 AGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGG 3360

Qy       3560 GGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCC 3619
             |||||||| |  ||||| | ||| |||||||| || ||||| ||||||||||||||||||
Db       3361 GGTGGGTGACGTAGGCCGTTAGCAGCTCTGCCATGTTGCCCTCAGGTGGGCCGCCACCCC 3420

Qy       3620 CTGACCTGCCTGGGTCCAAAGA 3641
             |||||||| ||||||||||||
Db       3421 TTGACCTGCATGGGTCCAAAGA 3442
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RESULT 13
ADS12778

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ID   ADS12778 standard; cDNA; 3810 BP.
XX
AC   ADS12778;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Human TRPM4a splicing variant cDNA sequence.
XX
KW   transient receptor potential cation channel; subfamily M; member 4;
KW   TRPM4; phospholipase A1-A; PLA1A; butyryl coenzyme A synthetase 1; BUCS1;
KW   prostate cancer; TRPM4a; gene; ss; splicing variant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             324. .3374
FT                   /*tag= a
FT                   /product= "Human TRPM4a splicing variant protein"
XX
PN   JP2004267118-A.
XX
PD   30-SEP-2004.
XX
PF   10-MAR-2003; 2003JP-00063578.
XX
PR   10-MAR-2003; 2003JP-00063578.
XX
PA   (SANY ) SANKYO CO LTD.
XX
DR   WPI; 2004-693915/68.
DR   P-PSDB; ADS12779.
XX
PT   Detecting prostatic cancer, comprises extracting RNA fractions from test
PT   substance of subject and normal human, measuring and analyzing the
PT   difference in e.g., phospholipase A1-A and butyryl coenzyme A synthetase
PT   expression levels.
XX
PS   Claim 1; SEQ ID NO 5; 126pp; Japanese.
XX
CC   The invention comprises a method for detecting prostatic cancer in a
CC   subject. The method involves measuring the expression levels of specific
CC   genes: transient receptor potential cation channel, subfamily M, member 4
CC   (TRPM4); phospholipase A1-A (PLA1A); and butyryl coenzyme A synthetase 1
CC   (BUCS1). The method of the invention is useful for the detection and
CC   treatment of prostate cancer. The present cDNA sequence encodes the human
CC   TRPM4a splicing variant protein of the invention.
XX
SQ   Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;
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  Query Match             93.9%;  Score 3421.2;  DB 13;  Length 3810;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 3429;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy        200 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCCGGCCGCAAGC 60

Qy        260 ACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCA 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        320 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGTGCTGGGGGGATCGGGGG 180

Qy        380 GCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCC 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGGGCTGGTGCGGGCTGCCC 240

Qy        440 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATGTTG 300

Qy        500 GTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGG 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGG 360

Qy        560 GTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGT 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGT 420

Qy        620 TCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACT 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCCTGGACT 480

Qy        680 ACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGA 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGGCTGCCTGGGGGGCGAGA 540

Qy        740 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGA 600

Qy        800 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGATGAGAAGATGTTGACGC 660

Qy        860 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGTGGCTGGCTCAGGGGGAG 720

Qy        920 CTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCA 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCA 780

Qy        980 GGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCC 1039
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Db      781 GGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAGGTCC 840
Qy     1040 TGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTG 1099
Db      841 TGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTG 900
Qy     1100 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGA 1159
Db      901 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGA 960
Qy     1160 GCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGG 1219
Db      961 GCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGG 1020
Qy     1220 ACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAG 1279
Db     1021 ACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAG 1080
Qy     1280 CTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCC 1339
Db     1081 CTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCC 1140
Qy     1340 ACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGG 1399
Db     1141 ACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGG 1200
Qy     1400 CGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCA 1459
Db     1201 CGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCA 1260
Qy     1460 AAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGC 1519
Db     1261 AAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGC 1320
Qy     1520 TGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACC 1579
Db     1321 TGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACC 1380
Qy     1580 CTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGC 1639
Db     1381 CTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGC 1440
Qy     1640 CGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCAC 1699
Db     1441 CGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCAC 1500
Qy     1700 TGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTT 1759
Db     1501 TGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTT 1560
Qy     1760 CCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTG 1819
Db     1561 CCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTG 1620
Qy     1820 AGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCT 1879
Db     1621 AGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCT 1680
Qy     1880 TTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCC 1939
Db     1681 TTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCCGTCGCTGCC 1740
Qy     1940 CGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCT 1999
Db     1741 CGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCTTCT 1800
Qy     2000 TTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCA 2059
Db     1801 TTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCA 1860
Qy     2060 CTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCC 2119
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Db     1861 CTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCC 1920
Qy     2120 TCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGG 2179
Db     1921 TCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGAGCTAGAGTTTGACATGG 1980
Qy     2180 ATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGC 2239
Db     1981 ATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCCAGCCGAGAAGACGCCGC 2040
Qy     2240 TGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCC 2299
Db     2041 TGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGGCCGCTGCGGGGGGCGCC 2100
Qy     2300 GGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACG 2359
Db     2101 GGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACG 2160
Qy     2360 TGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGC 2419
Db     2161 TGGTCAGCTACCTGCTGTTCTTGCTGCTTTTCTCGCGGGTGCTGCTCGTGGATTTCCAGC 2220
Qy     2420 CGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCG 2479
Db     2221 CGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCG 2280
Qy     2480 AGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGC 2539
Db     2281 AGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGC 2340
Qy     2540 CTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGT 2599
Db     2341 CTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGT 2400
Qy     2600 GCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTT 2659
Db     2401 GCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTT 2460
Qy     2660 TGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGC 2719
Db     2461 TGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGC 2520
Qy     2720 TTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGA 2779
Db     2521 TTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGA 2580
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Db     2581 TGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGG 2640
Qy     2840 CCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCT 2899
Db     2641 CCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCT 2700
Qy     2900 TCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCC 2959
Db     2701 TCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCC 2760
Qy     2960 TCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCC 3019
Db     2761 TCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCC 2820
Qy     3020 AGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCT 3079
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Qy     3080 TCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACAT 3139
Db     2881 TCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACAT 2940
Qy     3140 TCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCC 3199
Db     2941 TCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCC 3000
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Qy       3200 GGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCC 3259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 GGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCC 3060

Qy       3260 TCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCG 3319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCG 3120

Qy       3320 AGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGG 3379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 AGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGG 3180

Qy       3380 TGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGC 3439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 TGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGC 3240

Qy       3440 GTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCG 3499
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GTCTGGAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCG 3300

Qy       3500 AGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGG 3559
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Qy       3560 GGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCC 3619
             |||||||| |  ||||| | ||| |||||||| || ||||| ||||||||||||||||||
Db       3361 GGTGGGTGACGTAGGCCGTTAGCAGCTCTGCCATGTTGCCCTCAGGTGGGCCGCCACCCC 3420

Qy       3620 CTGACCTGCCTGGGTCCAAAGA 3641
              |||||||| ||||||||||||
Db       3421 TTGACCTGCATGGGTCCAAAGA 3442


RESULT 14
AAH76383
ID   AAH76383 standard; cDNA; 3900 BP.
XX
AC   AAH76383;
XX
DT   30-NOV-2001  (first entry)
XX
DE   Human TLCC polypeptide encoding cDNA.
XX
KW   TLCC; transient receptor potential; TRP; TRP-like calcium channel; human;
KW   hepatotropic; cardiant; antiarteriosclerotic; antiinflammatory; virucide;
KW   cytostatic; analgesic; cerebroprotective; nootropic; neuroprotective;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             138. .3527
FT                   /*tag= a
FT                   /product= "TLCC polypeptide"
FT                   /note= "coding sequence (AAH76384) specifically claimed"
XX
PN   WO200162794-A2.
XX
PD   30-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US005529.
XX
PR   22-FEB-2000; 2000US-00510706.
PR   31-MAY-2000; 2000US-00583373.
PR   08-AUG-2000; 2000US-00634669.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Glucksmann MA,  Curtis RAJ,  Lora JM;
XX
DR   WPI; 2001-557700/62.
DR   P-PSDB; AAB85974.
XX
PT   New isolated nucleic acid encoding a transient receptor potential-like
PT   calcium channel for identifying modulators that can be used to treat
PT   hepatic or cardiovascular disorders.
XX
PS   Claim 1; Fig 1A-D; 160pp; English.
XX
CC   The invention provides isolated nucleic acids encoding a human transient
CC   receptor potential (TRP) family member, called TRP-like calcium channel
CC   (TLCC) polypeptide. The TLCC polypeptide can be expressed by standard
CC   recombinant methodology. The TLCC polynucleotides and polypeptide are
CC   used to identify modulators that can be used to treat a hepatic or a
CC   cardiovascular disorder, such as liver fibrosis or atherosclerosis. Other
CC   disorders that can be treated are hepatitis, liver tumours, cirrhosis of
CC   the liver, hemochromatosis, liver parasite induced disorders, central
CC   nervous system disorders, pain disorders, or disorders of cellular
CC   growth, differentiation or migration. The TLCC polynucleotides,
CC   polypeptide, protein homologs and antibodies to the proteins can be used
CC   in predictive medicine (e.g. diagnostic assays, prognostic assays,
CC   monitoring clinical trials and pharmacogenetics). Anti-TLCC antibodies
CC   can isolate TLCC proteins, regulate the bioavailablility of TLCC
CC   proteins, and modulate TLCC activity. The present sequence represents a
CC   cDNA encoding the human TLCC polypeptide
XX
SQ   Sequence 3900 BP; 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;

  Query Match             92.7%;  Score 3374.4;  DB 5;  Length 3900;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 3384;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy        243 GGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGC 302
              | |  |||  | || |       | ||||||||||||||||||||||||||||||||||
Db        125 GTGCCCCGCTCCCATGTGTCCACAGTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGC 184

Qy        303 AGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGT 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 AGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGT 244

Qy        363 GCTGGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGG 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GCTGGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGG 304

Qy        423 GCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGG 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGG 364

Qy        483 CATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCAC 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 CATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCAC 424

Qy        543 CAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCAT 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 CAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCAT 484

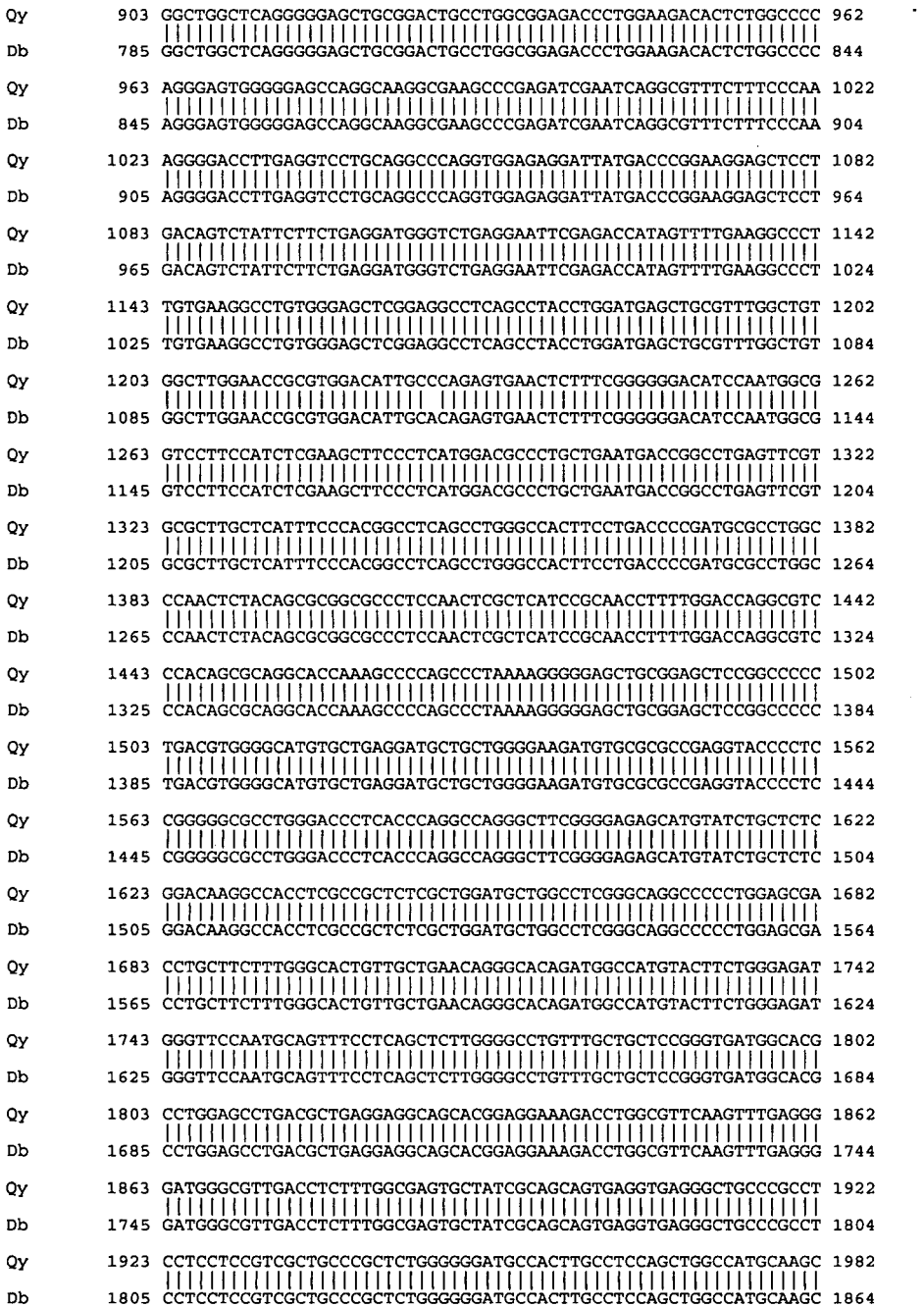
Qy        603 CAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGT 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGT 544

Qy        663 CCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGG 722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 CCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGG 604

Qy        723 CTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAA 782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 CTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAA 664

Qy        783 GACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGA 842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 GACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGA 724

Qy        843 TGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGT 902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 TGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGT 784
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Qy 903 GGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCC 962
Db 785 GGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCC 844
Qy 963 AGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAA 1022
Db 845 AGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAA 904
Qy 1023 AGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCT 1082
Db 905 AGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCT 964
Qy 1083 GACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCT 1142
Db 965 GACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCT 1024
Qy 1143 TGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGT 1202
Db 1025 TGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGT 1084
Qy 1203 GGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCG 1262
Db 1085 GGCTTGGAACCGCGTGGACATTGCACAGAGTGAACTCTTTCGGGGGGACATCCAATGGCG 1144
Qy 1263 GTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGT 1322
Db 1145 GTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGT 1204
Qy 1323 GCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGC 1382
Db 1205 GCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGC 1264
Qy 1383 CCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTC 1442
Db 1265 CCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCCGCAACCTTTTGGACCAGGCGTC 1324
Qy 1443 CCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGGCCCCC 1502
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Qy 1563 CGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTC 1622
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Qy 1623 GGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGA 1682
Db 1505 GGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGA 1564
Qy 1683 CCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGAT 1742
Db 1565 CCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGAT 1624
Qy 1743 GGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACG 1802
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Qy 1803 CCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGG 1862
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Db 1745 GATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCT 1804
Qy 1923 CCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGC 1982
Db 1805 CCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGC 1864
Qy 1983 TGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTG 2042
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Qy 2043 GGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCC 2102
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Qy 2223 AGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGG 2282
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Qy 2283 CCGCTGCGGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGAC 2342
Db 2165 CCGCTGCGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGAC 2224
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Db 2225 CATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCT 2284
Qy 2403 GCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGC 2462
Db 2285 GCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGC 2344
Qy 2463 TTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGC 2522
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Qy 2583 CGACAGCTGGAACCAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTG 2642
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Qy 2643 CCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGT 2702
Db 2525 CCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGT 2584
Qy 2703 TTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGT 2762
Db 2585 TTTCACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGT 2644
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Db 2645 CATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCT 2704
Qy 2823 GGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAG 2882
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Qy 2883 TATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGA 2942
Db 2765 TATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGA 2824
Qy 2943 GGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGC 3002
Db 2825 GGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGC 2884
Qy 3003 ACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGT 3062
Db 2885 ACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGT 2944
Qy 3063 GCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGC 3122

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2945 GCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGC 3004

Qy       3123 CATGTTCAGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCA 3182
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3183 GCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGT 3242
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3065 GCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGT 3124

Qy       3243 CATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCC 3302
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3303 GTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCT 3362
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3185 GTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCT 3244

Qy       3363 GCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCG 3422
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3245 GCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCG 3304

Qy       3423 GGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACA 3482
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3483 GCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCA 3542
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Db       3365 GCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCA 3424

Qy       3543 GTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCC 3602
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Db       3425 GTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCC 3484

Qy       3603 AGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGAC 3642
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Db       3485 AGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGAC 3524


RESULT 15
ABS58041
ID   ABS58041 standard; cDNA; 3900 BP.
XX
AC   ABS58041;
XX
DT   14-FEB-2003  (first entry)
XX
DE   Human transient receptor potential (TRP)-like calcium channel (TLCC).
XX
KW   Human; gene; ss; transient receptor potential-like calcium channel; TRP;
KW   TLCC; 18607; calcium signalling; growth; differentiation;
KW   capacitative calcium channel; store-operated calcium channel; SOC;
KW   plasma membrane; calcium ion; cytosol; modulator; membrane excitability;
KW   action potential; excitation; neurite outgrowth; synaptogenesis;
KW   signal transduction; angiogenesis; cell proliferation; vascular tone;
KW   gene therapy; diagnosis; cardiovascular disorder; atherosclerosis;
KW   restenosis; endothelial cell disorder; tumour metastasis; psoriasis;
KW   rheumatoid arthritis; diabetes; hepatic disorder; hepatitis; cirrhosis;
KW   central nervous system disorder; Alzheimer's disease;
KW   Parkinson's disease; multiple sclerosis; epilepsy; cancer;
KW   cellular proliferation disorder; migration disorder; therapeutic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1. .137
FT                   /*tag=  a
FT   CDS             138. .3390
FT                   /*tag=  b
FT                   /product= "TLCC"
FT                   /note= "This CDS is specifically claimed in claim 1"
FT   3'UTR           3391. .3900
FT                   /*tag=  c
XX
PN   US2002142377-A1.
XX
PD   03-OCT-2002.
XX
PF   20-FEB-2001; 2001US-00789481.
XX
PR   22-FEB-2000; 2000US-00510706.
PR   31-MAY-2000; 2000US-00583373.
PR   08-AUG-2000; 2000US-00634669.
XX
PA   (GLUC/) GLUCKSMANN M A.
PA   (CURT/) CURTIS R A J.
PA   (LORA/) LORA J M.
XX
PI   Glucksmann MA,  Curtis RAJ,  Lora JM;
XX
DR   WPI; 2003-102516/09.
DR   P-PSDB; ABG72088.
XX
PT   Isolated transient receptor potential-like calcium channel polypeptide,
PT   useful for treating cardiovascular, hepatic, central nervous system
PT   disorders, pain, cellular proliferation, or migration disorder.
XX
PS   Claim 1; Fig 1; 80pp; English.
XX
CC   The invention discloses an isolated transient receptor potential (TRP)-
CC   like calcium channel (TLCC) polypeptide (18607). Calcium signalling has
CC   been implicated in the regulation of a variety of cellular responses,
CC   such as growth and differentiation. TLCC is a member of the capacitative
CC   calcium channel group or store-operated calcium channel (SOC) which is
CC   activated in the plasma membrane to import calcium ions from the
CC   extracellular environment to the cytosol. The nucleic acids, polypeptides
CC   and antibodies of TLCC are useful for detecting its presence in a sample,
CC   for identifying a compound which binds to it and identifying a compound
CC   which modulates its activity. Modulators of TLCC can be used to modulate
CC   membrane excitability, wave forms and frequencies of action potentials,
CC   thresholds of excitation, neurite outgrowth and synaptogenesis, signal
CC   transduction, angiogenesis, endothelial cell proliferation and vascular
CC   tone. The nucleic acid and polypeptide are also useful (using gene
CC   therapy) for diagnosing and treating cardiovascular disorders, such as
CC   atherosclerosis and restenosis, endothelial cell disorders, such as
CC   tumour metastasis, psoriasis, rheumatoid arthritis and diabetes, hepatic
CC   disorders such hepatitis and cirrhosis, central nervous system disorders,
CC   such as Alzheimer's disease, Parkinson's disease, multiple sclerosis and
CC   epilepsy, cellular proliferation disorders, such as cancer, and growth,
CC   differentiation or migration disorders. TLCC can also be used in
CC   predictive medicine (e.g. diagnostic assays, prognostic assays,
CC   monitoring clinical trials and pharmacogenomics) and in methods of
CC   treatment (e.g. therapeutic and prophylactic). The sequence presented is
CC   the human TLCC, 18607, cDNA
XX
SQ   Sequence 3900 BP; 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;

  Query Match             92.7%;  Score 3374.4;  DB 8;  Length 3900;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 3384;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy        243 GGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGC 302
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Qy        303 AGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTCAGT 362
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Qy        363 GCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGG 422
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Db        245 GCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCGTGG 304

Qy        423 GCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGG 482
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Db        305 GCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGG 364

Qy        483 CATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCAC 542
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Qy        543 CAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCAT 602
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Qy        603 CAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGGGT 662
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Qy        663 CCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACGGCACACACGG 722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        723 CTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCTCACAGCAGAA 782
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Qy        783 GACGGGCGTGGGAGGGACTGGAATTGACATCCCTGTCCTGCTCCTCCTGATTGATGGTGA 842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        843 TGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCCTCGT 902
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Qy        903 GGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCC 962
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Qy        963 AGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAA 1022
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Qy       1023 AGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCT 1082
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Db        905 AGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCT 964

Qy       1083 GACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCT 1142
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Db        965 GACAGTCTATTCTTCTGAGGATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCT 1024

Qy       1143 TGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGT 1202
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Qy       1203 GGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCTTTCGGGGGGACATCCAATGGCG 1262
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Qy       1263 GTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGCTGAATGACCGGCCTGAGTTCGT 1322
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Qy       1503 TGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTC 1562
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Qy       1563 CGGGGGCGCCTGGGACCCTCACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTC 1622
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Qy       1683 CCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGAT 1742
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Qy       1743 GGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACG 1802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1625 GGGTTCCAATGCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACG 1684

Qy       1803 CCTGGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGG 1862
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Qy       1863 GATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCT 1922
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Qy       1923 CCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGC 1982
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Db       1805 CCTCCTCCGTCGCTGCCCGCTCTGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGC 1864

Qy       1983 TGACGCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTG 2042
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Qy       2043 GGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCC 2102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1925 GGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCC 1984

Qy       2103 ACTCATCTACACCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCCACACGGGAGGA 2162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2163 GCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTCGGGACGGCGGACCC 2222
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Qy       2223 AGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTTGCTGCGGGGG 2282
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Qy       2283 CCGCTGCGGGGGGGCGCCGGTGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGAC 2342
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Db       2225 CATCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCCTGCTGCTTTTCTCGCGGGTGCT 2284

Qy       2403 GCTCGTGGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGC 2462
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Qy       2463 TTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGC 2522
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Qy       2643 CCGGCTGACCCCGGGTTTGTACCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGT 2702
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Qy       3003 ACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGT 3062
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Qy       3063 GCTGCTCCTCGTCATCTTCCTGCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGC 3122
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Qy       3303 GTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCT 3362
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Qy       3483 GCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCA 3542
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Db       3365 GCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCA 3424

Qy       3543 GTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCC 3602
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Db       3425 GTGTAGCCGCGTCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCC 3484

Qy       3603 AGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGAC 3642
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Db       3485 AGGTGGGCCGCCACCCCCTGACCTGCCTGGGTCCAAAGAC 3524
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Search completed: June 12, 2005, 18:59:36
Job time : 1225.46 secs

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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 18:12:43 ; Search time 393.939 Seconds
(without alignments)
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Perfect score: 3642
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1158	31.8	1524	3	US-09-020-956-109	Sequence 109, App
2	1158	31.8	1524	3	US-09-030-607-109	Sequence 109, App
3	1158	31.8	1524	3	US-09-439-313-109	Sequence 109, App
4	1158	31.8	1524	3	US-09-352-616A-109	Sequence 109, App
5	1158	31.8	1524	3	US-09-232-149A-109	Sequence 109, App
6	1158	31.8	1524	4	US-09-159-812-109	Sequence 109, App
7	1158	31.8	1524	4	US-09-636-215-109	Sequence 109, App
8	1158	31.8	1524	4	US-09-685-166A-109	Sequence 109, App
9	1158	31.8	1524	4	US-09-115-453-109	Sequence 109, App
10	1158	31.8	1524	4	US-09-688-489-109	Sequence 109, App
11	1158	31.8	1524	4	US-09-679-426-109	Sequence 109, App
12	1158	31.8	1524	4	US-09-759-143-109	Sequence 109, App
13	1158	31.8	1524	4	US-09-651-236-109	Sequence 109, App
14	1095.2	30.1	1297	2	US-08-727-688-9	Sequence 9, Appli
15	815.8	22.4	3498	4	US-09-949-016-1003	Sequence 1003, Ap
16	814.2	22.4	3498	4	US-09-949-016-5521	Sequence 5521, Ap
17	428.6	11.8	6220	4	US-09-600-087-1	Sequence 1, Appli
18	428.6	11.8	6220	4	US-09-949-016-470	Sequence 470, App
19	427	11.7	6221	4	US-09-949-016-5229	Sequence 5229, Ap
20	358	9.8	384	3	US-09-030-607-185	Sequence 185, App
21	358	9.8	384	3	US-09-439-313-185	Sequence 185, App
22	358	9.8	384	3	US-09-352-616A-185	Sequence 185, App
23	358	9.8	384	3	US-09-232-149A-185	Sequence 185, App
24	358	9.8	384	4	US-09-159-812-185	Sequence 185, App
25	358	9.8	384	4	US-09-636-215-185	Sequence 185, App
26	358	9.8	384	4	US-09-685-166A-185	Sequence 185, App
27	358	9.8	384	4	US-09-115-453-185	Sequence 185, App
28	358	9.8	384	4	US-09-688-489-185	Sequence 185, App
29	358	9.8	384	4	US-09-679-426-185	Sequence 185, App
30	358	9.8	384	4	US-09-759-143-185	Sequence 185, App
31	358	9.8	384	4	US-09-651-236-185	Sequence 185, App
32	348.6	9.6	380	3	US-09-020-956-84	Sequence 84, Appl
33	348.6	9.6	380	3	US-09-030-607-84	Sequence 84, Appl
34	348.6	9.6	380	3	US-09-439-313-84	Sequence 84, Appl
35	348.6	9.6	380	3	US-09-352-616A-84	Sequence 84, Appl
36	348.6	9.6	380	3	US-09-232-149A-84	Sequence 84, Appl
37	348.6	9.6	380	4	US-09-159-812-84	Sequence 84, Appl
38	348.6	9.6	380	4	US-09-636-215-84	Sequence 84, Appl
39	348.6	9.6	380	4	US-09-685-166A-84	Sequence 84, Appl
40	348.6	9.6	380	4	US-09-115-453-84	Sequence 84, Appl
41	348.6	9.6	380	4	US-09-688-489-84	Sequence 84, Appl
42	348.6	9.6	380	4	US-09-679-426-84	Sequence 84, Appl
43	348.6	9.6	380	4	US-09-759-143-84	Sequence 84, Appl
44	348.6	9.6	380	4	US-09-651-236-84	Sequence 84, Appl
45	304	8.3	367	2	US-08-727-688-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-09-020-956-109
; Sequence 109, Application US/09020956
; Patent No. 6261562
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Jiangchun
;    APPLICANT:  Dillin, Davin C.
;    TITLE OF INVENTION:  COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
;    NUMBER OF SEQUENCES:  178
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/020,956
;      FILING DATE:  09-FEB-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.427C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  109:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1524 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-09-020-956-109

  Query Match           31.8%;  Score 1158;  DB 3;  Length 1524;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-264;
  Matches 1158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69
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Qy       2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2605 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2664
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2665 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2724
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       2845 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2904
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2905 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2964
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       3025 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3084
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3145 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3204
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3384
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Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3445 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3504
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Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3505 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3564
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3565 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3624
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3625 CTGCCTGGGTCCAAAGAC 3642
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Db       1150 CTGCCTGGGTCCAAAGAC 1167
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RESULT 2
US-09-030-607-109
; Sequence 109, Application US/09030607
; Patent No. 6262245
;  GENERAL INFORMATION:
;    APPLICANT:  Xu, Jiangchun
;    APPLICANT:  Dillon, Davin C.
;    TITLE OF INVENTION:  COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
;    NUMBER OF SEQUENCES:  224
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/030,607
;      FILING DATE:  25-FEB-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.427C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  109:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1524 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-09-030-607-109

  Query Match             31.8%;  Score 1158;  DB 3;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-264;
  Matches 1158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy       2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
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Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2605 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2664
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2665 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2724
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
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Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       2845 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2904
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2905 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2964
Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       3025 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3084
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3145 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3204
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3384
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3445 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3504
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3505 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3564
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3565 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3624
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Qy       3625 CTGCCTGGGTCCAAAGAC 3642
Db       1150 CTGCCTGGGTCCAAAGAC 1167
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RESULT 3
US-09-439-313-109
; Sequence 109, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan Louise
;  APPLICANT:  Jiang Yuqui
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Kalos, Michael
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Retter, Mark
;  APPLICANT:  Solk, John
;  APPLICANT:  Day, Craig
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C9
;  CURRENT APPLICATION NUMBER: US/09/439,313
;  CURRENT FILING DATE:  1999-11-12
;  NUMBER OF SEQ ID NOS: 575
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-439-313-109

  Query Match             31.8%;  Score 1158;  DB 3;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-264;
  Matches 1158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy       2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2605 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2664
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2665 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2724
Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       2845 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2904
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2905 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2964
Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       3025 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3084
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3145 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3204
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
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Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3384
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Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3445 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3504
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3505 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3564
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3565 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3624
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Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3625 CTGCCTGGGTCCAAAGAC 3642
                 ||||||||||||||||||
Db       1150 CTGCCTGGGTCCAAAGAC 1167


RESULT 4
US-09-352-616A-109
; Sequence 109, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Harlocker, Susan Louise
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Mitcham, Jennifer Lynn
;  TITLE OF INVENTION:  COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
;  TITLE OF INVENTION:  OF PROSTATE CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE:  210121.427C8
;  CURRENT APPLICATION NUMBER: US/09/352,616A
;  CURRENT FILING DATE:  1999-07-13
;  NUMBER OF SEQ ID NOS:  472
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-352-616A-109

  Query Match             31.8%;  Score 1158;  DB 3;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-264;
  Matches 1158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
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Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy       2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
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Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2605 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2664
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Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2665 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2724
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Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
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Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
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Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

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Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
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Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
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Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3145 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3204
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
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Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3384
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Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

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Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3625 CTGCCTGGGTCCAAAGAC 3642
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RESULT 5
US-09-232-149A-109
; Sequence 109, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer Lynn
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
;  TITLE OF INVENTION:  CANCER AND METHODS FOR THEIR USE
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;  FILE REFERENCE: 210121.427C6
;  CURRENT APPLICATION NUMBER: US/09/232,149A
;  CURRENT FILING DATE:  1999-01-15
;  NUMBER OF SEQ ID NOS: 338
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-232-149A-109

  Query Match             31.8%;  Score 1158;  DB 3;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-264;
  Matches 1158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
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Qy       2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
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Qy       2605 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2664
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Qy       2665 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2724
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Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
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Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
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Qy       2845 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2904
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Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2905 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2964
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Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
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Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
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Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3145 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3204
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Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
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Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
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Qy       3625 CTGCCTGGGTCCAAAGAC 3642
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RESULT 6
US-09-159-812-109
; Sequence 109, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT: Dillon, Davin C.
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
;  TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.428C5
;  CURRENT APPLICATION NUMBER: US/09/159,812A
;  CURRENT FILING DATE: 1998-09-23
;  NUMBER OF SEQ ID NOS: 306
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-159-812-109

  Query Match             31.8%;  Score 1158;  DB 4;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-264;
  Matches 1158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
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Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

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Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
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Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

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Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
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Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
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Db       1150 CTGCCTGGGTCCAAAGAC 1167


RESULT 7
US-09-636-215-109
; Sequence 109, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.42717C17
;  CURRENT APPLICATION NUMBER: US/09/636,215
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS:  852
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-636-215-109

  Query Match             31.8%;  Score 1158;  DB 4;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-264;
  Matches 1158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
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Db          10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy       2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
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Qy       2665 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2724
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Db         190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       2845 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2904
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2905 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2964
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       3025 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3084
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3145 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3204
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789
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Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3384
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3445 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3504
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3505 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3564
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3565 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3624
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Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3625 CTGCCTGGGTCCAAAGAC 3642
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Db       1150 CTGCCTGGGTCCAAAGAC 1167


RESULT 8
US-09-685-166A-109
; Sequence 109, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C21
;  CURRENT APPLICATION NUMBER: US/09/685,166A
;  CURRENT FILING DATE:  2000-10-10
;  NUMBER OF SEQ ID NOS: 898
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-685-166A-109

  Query Match             31.8%;  Score 1158;  DB 4;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-264;
  Matches 1158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
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Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy       2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2605 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2664
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2665 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2724
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Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
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Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
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Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       2845 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2904
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Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2905 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2964
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Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       3025 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3084
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3145 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3204
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
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Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3384
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Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3445 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3504
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Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3505 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3564
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Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3565 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3624
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3625 CTGCCTGGGTCCAAAGAC 3642
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Db       1150 CTGCCTGGGTCCAAAGAC 1167


RESULT 9
US-09-115-453-109
; Sequence 109, Application US/09115453B
; Patent No. 6657056
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT: Dillon, Davin C.
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
;  TITLE OF INVENTION: METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.427C4
;  CURRENT APPLICATION NUMBER: US/09/115,453B
;  CURRENT FILING DATE: 1998-07-14
;  NUMBER OF SEQ ID NOS: 228
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-115-453-109

  Query Match             31.8%;  Score 1158;  DB 4;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-264;
  Matches 1158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy       2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2605 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2664
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2665 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2724
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Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
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Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       2845 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2904
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2905 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2964
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Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       3025 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3084
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3145 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3204
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
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Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3384
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Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3445 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3504
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3505 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3564
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Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3565 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3624
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3625 CTGCCTGGGTCCAAAGAC 3642
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Db       1150 CTGCCTGGGTCCAAAGAC 1167


RESULT 10
US-09-688-489-109
; Sequence 109, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer Lynn
;  TITLE OF INVENTION:  COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
;  TITLE OF INVENTION:  CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE:  210121.427D2
;  CURRENT APPLICATION NUMBER: US/09/688,489
;  CURRENT FILING DATE:  2000-10-13
;  NUMBER OF SEQ ID NOS:  338
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-688-489-109

  Query Match             31.8%;  Score 1158;  DB 4;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-264;
  Matches 1158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
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Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy       2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2605 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2664
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2665 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2724
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Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
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Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       2845 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2904
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Qy       2905 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2964
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       3025 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3084
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3145 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3204
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3384
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3445 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3504
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3505 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3564
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3565 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3624
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3625 CTGCCTGGGTCCAAAGAC 3642
                ||||||||||||||||||
Db       1150 CTGCCTGGGTCCAAAGAC 1167


RESULT 11
US-09-679-426-109
; Sequence 109, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C20
;  CURRENT APPLICATION NUMBER: US/09/679,426
;  CURRENT FILING DATE:  2000-10-02
;  NUMBER OF SEQ ID NOS:  895
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-679-426-109

  Query Match             31.8%;  Score 1158;  DB 4;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-264;
  Matches 1158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy       2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
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Db          70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2605 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2664
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2665 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2724
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Db         190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
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Db         250 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 309

Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

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Db         430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
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Db         490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

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Db         550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609
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Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3145 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3204
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
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Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3384
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Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
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Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3445 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3504
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Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

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Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3565 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3624
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Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3625 CTGCCTGGGTCCAAAGAC 3642
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Db       1150 CTGCCTGGGTCCAAAGAC 1167
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RESULT 12
US-09-759-143-109
; Sequence 109, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C23
;  CURRENT APPLICATION NUMBER: US/09/759,143
;  CURRENT FILING DATE:  2001-01-12
;  NUMBER OF SEQ ID NOS:  934
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-759-143-109

  Query Match             31.8%;  Score 1158;  DB 4;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-264;
  Matches 1158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
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Qy       2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
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Db         70 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 129

Qy       2605 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 2664
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Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

Qy       2665 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 2724
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Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
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Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
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Db        310 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 369

Qy       2845 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2904
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Db        370 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 429

Qy       2905 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2964
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Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
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Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

Qy       3025 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 3084
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCTG 609

Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 669

Qy       3145 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 3204
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3384
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3445 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3504
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Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3505 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3564
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Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3565 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3624
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Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3625 CTGCCTGGGTCCAAAGAC 3642
                 ||||||||||||||||||
Db       1150 CTGCCTGGGTCCAAAGAC 1167


RESULT 13
US-09-651-236-109
; Sequence 109, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.42718C18
;  CURRENT APPLICATION NUMBER: US/09/651,236
;  CURRENT FILING DATE:  2000-08-29
;  NUMBER OF SEQ ID NOS:  865
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 109
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-651-236-109

  Query Match             31.8%;  Score 1158;  DB 4;  Length 1524;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-264;
  Matches 1158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2485 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 2544
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Db         10 CTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGGCCCCGGGCCTGGC 69

Qy       2545 CATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGCGAC 2604
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Db        130 CTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTAC 189

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Db        190 CACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCAC 249

Qy       2725 ATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAG 2784
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Qy       2785 GACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACG 2844
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Qy       2845 GAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTAC 2904
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Qy       2905 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 2964
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Db        430 CGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATG 489

Qy       2965 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 3024
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Db        490 GAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCG 549

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Qy       3085 CTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGGC 3144
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAA 729

Qy       3205 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 3264
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTG 789

Qy       3265 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 3324
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCAT 849

Qy       3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 3384
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCAT 909

Qy       3385 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 3444
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTG 969

Qy       3445 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3504
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 1029

Qy       3505 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 3564
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTGG 1089

Qy       3565 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 3624
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 GTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGAC 1149

Qy       3625 CTGCCTGGGTCCAAAGAC 3642
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RESULT 14
US-08-727-688-9
; Sequence 9, Application US/08727688
; Patent No. 5919638
;  GENERAL INFORMATION:
;     APPLICANT:  Russell, John C.
;     TITLE OF INVENTION:  Reagents and Methods for Detecting Prostate Tumors
;     NUMBER OF SEQUENCES:  36
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Abbott Laboratories
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;      STREET:  100 Abbott Park Road D377/AP6D
;      CITY:  Abbott Park
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/727,688
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Porembski, Priscilla E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5967.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (847) 937-0378
;      TELEFAX:  (847) 938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1297 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-727-688-9

  Query Match             30.1%;  Score 1095.2;  DB 2;  Length 1297;
  Best Local Similarity   98.7%;  Pred. No. 1.2e-249;
  Matches 1144;  Conservative    0;  Mismatches   11;  Indels    4;  Gaps    4;

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Db          1 TGCGCNGGAGCCTGAGCGGAGGGTGTGCGCAGCCTCGCCAGCGGGGGCCCCGGGCTGNGC 60

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              || |||||||||||||||||||| |  ||||||||||||||||||||||||||||||||
Db         61 CATTGCCTCACTGAGCCAGCGCCTGC-CTNCTACCTCGCCGACAGCTGGAACCAGTGCGA 119

Qy       2604 CCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTA 2663
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Db        120 CCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTA 179

Qy       2664 CCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCA 2723
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Db        180 CCACCTGGGCCGCACTGTCCTCTGCATCGACTTCATGGTTTTCACGGTGCGGCTGCTTCA 239

Qy       2724 CATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAA 2783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 CATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAA 299

Qy       2784 GGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCAC 2843
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Db        300 GGACGTGTTCTTCTTCCTCTTCTTCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCAC 359

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Qy       3024 GGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCCT 3083
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Qy       3084 GCTCGTGGCCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAGTTACACATTCGG 3143
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Qy       3144 CAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGA 3203
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Qy       3264 GCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCA 3323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 GCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCCAGCCGTCCTCCCCGGCCCTCGAGCA 838

Qy       3324 TTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCA 3383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 TTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCA 898

Qy       3384 TAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCT 3443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 TAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCT 958

Qy       3444 GAAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTA 3503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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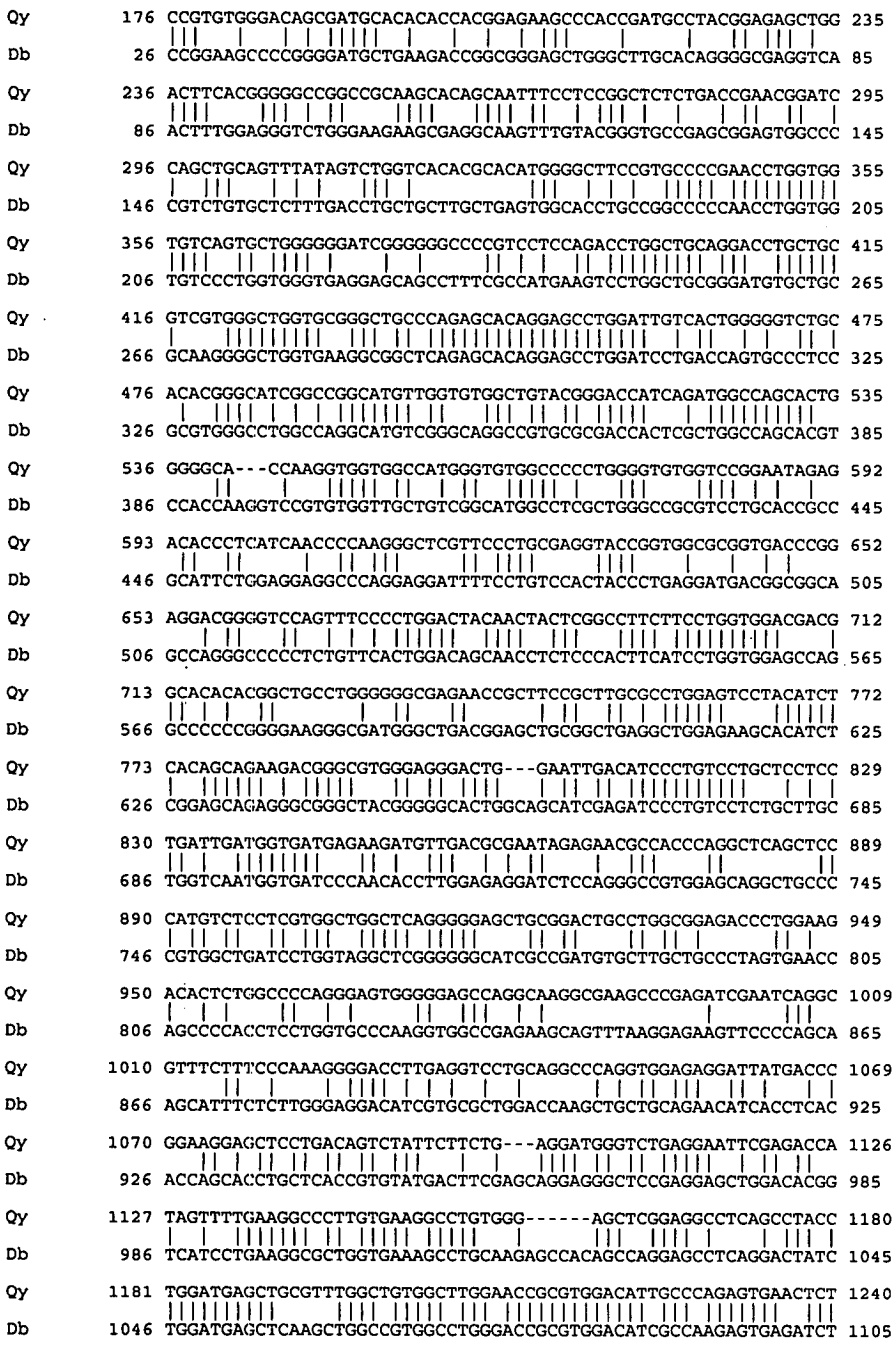
Qy       3504 CGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTG 3563
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Db       1019 CGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCCTGGGGTG 1078

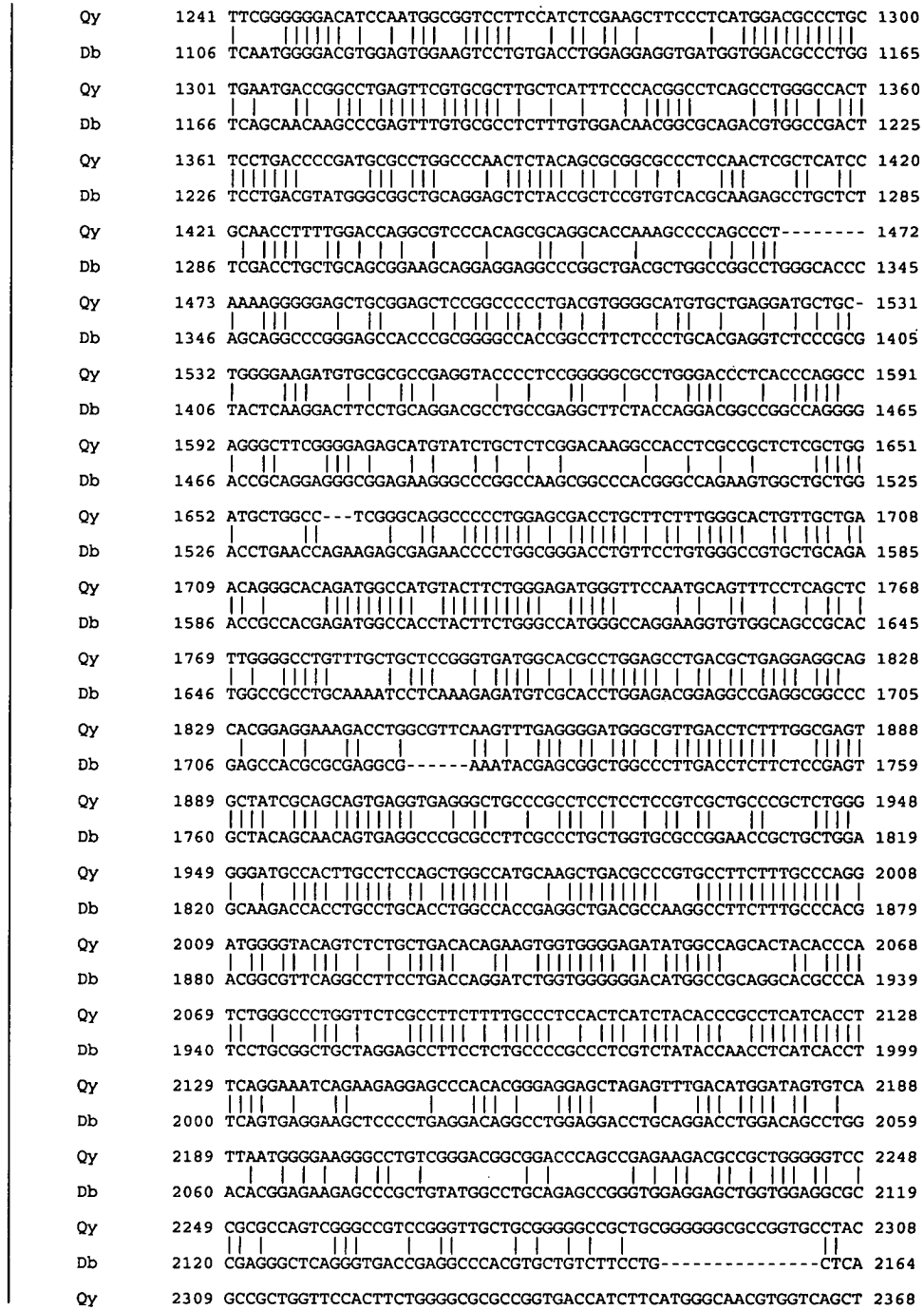
Qy       3564 GGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGA 3623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 GGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCCAGGTGGGCCGCCACCCCCTGA 1138

Qy       3624 CCTGCCTGGGTCCAAAGAC 3642
              |||||||||||||||||||
Db       1139 CCTGCCTGGGTCCAAAGAC 1157


RESULT 15
US-09-949-016-1003
; Sequence 1003, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1003
;   LENGTH: 3498
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-1003

  Query Match             22.4%;  Score 815.8;  DB 4;  Length 3498;
  Best Local Similarity   55.6%;  Pred. No. 3.3e-183;
  Matches 1916;  Conservative    0;  Mismatches 1407;  Indels  126;  Gaps   13;
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Qy 176 CCGTGTGGGACAGCGATGCACACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGG 235
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Qy 236 ACTTCACGGGGGCCGGCCGCAAGCACAGCAATTTCCTCCGGCTCTCTGACCGAACGGATC 295
Db 86 ACTTTGGAGGGTCTGGGAAGAAGCGAGGCAAGTTTGTACGGGTGCCGAGCGGAGTGGCCC 145
Qy 296 CAGCTGCAGTTTATAGTCTGGTCACACGCACATGGGGCTTCCGTGCCCCGAACCTGGTGG 355
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Qy 356 TGTCAGTGCTGGGGGGATCGGGGGGCCCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGC 415
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Qy 416 GTCGTGGGCTGGTGCGGGCTGCCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGC 475
Db 266 GCAAGGGGCTGGTGAAGGCGGCTCAGAGCACAGGAGCCTGGATCCTGACCAGTGCCCTCC 325
Qy 476 ACACGGGCATCGGCCGGCATGTTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTG 535
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Qy 536 GGGGCA---CCAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGTGTGGTCCGGAATAGAG 592
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Qy 593 ACACCCTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCCGG 652
Db 446 GCATTCTGGAGGAGGCCCAGGAGGATTTTCCTGTCCACTACCCTGAGGATGACGGCGGCA 505
Qy 653 AGGACGGGGTCCAGTTTCCCCTGGACTACAACTACTCGGCCTTCTTCCTGGTGGACGACG 712
Db 506 GCCAGGGCCCCCTCTGTTCACTGGACAGCAACCTCTCCCACTTCATCCTGGTGGAGCCAG 565
Qy 713 GCACACACGGCTGCCTGGGGGGCGAGAACCGCTTCCGCTTGCGCCTGGAGTCCTACATCT 772
Db 566 GCCCCCCGGGGAAGGGCGATGGGCTGACGGAGCTGCGGCTGAGGCTGGAGAAGCACATCT 625
Qy 773 CACAGCAGAAGACGGGCGTGGGAGGGACTG---GAATTGACATCCCTGTCCTGCTCCTCC 829
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Qy 830 TGATTGATGGTGATGAGAAGATGTTGACGCGAATAGAGAACGCCACCCAGGCTCAGCTCC 889
Db 686 TGGTCAATGGTGATCCCAACACCTTGGAGAGGATCTCCAGGGCCGTGGAGCAGGCTGCCC 745
Qy 890 CATGTCTCCTCGTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCTGGAAG 949
Db 746 CGTGGCTGATCCTGGTAGGCTCGGGGGGCATCGCCGATGTGCTTGCTGCCCTAGTGAACC 805
Qy 950 ACACTCTGGCCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGC 1009
Db 806 AGCCCCACCTCCTGGTGCCCAAGGTGGCCGAGAAGCAGTTTAAGGAGAAGTTCCCCAGCA 865
Qy 1010 GTTTCTTTCCCAAAGGGGACCTTGAGGTCCTGCAGGCCCAGGTGGAGAGGATTATGACCC 1069
Db 866 AGCATTTCTCTTGGGAGGACATCGTGCGCTGGACCAAGCTGCTGCAGAACATCACCTCAC 925
Qy 1070 GGAAGGAGCTCCTGACAGTCTATTCTTCTG---AGGATGGGTCTGAGGAATTCGAGACCA 1126
Db 926 ACCAGCACCTGCTCACCGTGTATGACTTCGAGCAGGAGGGCTCCGAGGAGCTGGACACGG 985
Qy 1127 TAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGG------AGCTCGGAGGCCTCAGCCTACC 1180
Db 986 TCATCCTGAAGGCGCTGGTGAAAGCCTGCAAGAGCCACAGCCAGGAGCCTCAGGACTATC 1045
Qy 1181 TGGATGAGCTGCGTTTGGCTGTGGCTTGGAACCGCGTGGACATTGCCCAGAGTGAACTCT 1240
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Qy 1241 TTCGGGGGGACATCCAATGGCGGTCCTTCCATCTCGAAGCTTCCCTCATGGACGCCCTGC 1300
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Qy 1301 TGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCCACGGCCTCAGCCTGGGCCACT 1360
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Qy 1361 TCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACTCGCTCATCC 1420
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Qy 1532 TGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCTCACCCAGGCC 1591
Db 1406 TACTCAAGGACTTCCTGCAGGACGCCTGCCGAGGCTTCTACCAGGACGGCCGGCCAGGGG 1465
Qy 1592 AGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGG 1651
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Job time : 398.939 secs